

STIC-Biotech/ChemLib

137502

From: Chernyshev, Olga
Sent: Tuesday, November 09, 2004 3:10 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request

Please search US case 09/876,813

SEQ ID NO: 2, full length and fragment 258-370 and

SEQ ID NO: 6, full length and fragment 748-1110.

Regular and pending databases.

Thank you very much!

Olga N. Chernyshev, Ph.D.

AU 1646

4D84

2-0870

mail 4C70

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(STIC)

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Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 15:30:26 ; Search time 5888.35 Seconds
(without alignments)
6869.174 Million cell updates/sec

Title: US-09-876-813-6
Perfect score: 1110
Sequence: 1 atgcagymgynhcnatcttgc.....gymenwamgncnccmgn 1110

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

EST:
1: gb_scat1.*
2: gb_scat2.*
3: gb_hrc.*
4: gb_scat3.*
5: gb_scat4.*
6: gb_scat5.*
7: gb_scat6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798	71.9	3739	3	AF113216 Homo sapi
2	757.4	68.2	1095	9	AY419997 Homo sapi
3	756.8	68.2	1095	9	AY419998 Homo sapi
4	714.8	64.4	1797	3	AK003359 Mus muscu
5	674.2	60.7	1095	9	AY419999 Mus muscu
6	466.2	42.0	819	5	BU359805 Mus muscu
7	459	41.4	799	2	BE914552 BE914552
8	453	40.8	1044	5	BU213231 BU213231
9	440	39.6	727	5	BU326159 BU326159
10	439.4	39.6	985	5	BU311960 BU311960
11	427.4	38.5	798	5	BU404150 BU404150
12	422.8	38.1	921	5	BU15557 BU15557
13	406.6	36.6	723	4	BT689894 BT689894
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15	382.6	34.5	774	5	BU290871 BU290871
16	375.2	33.8	645	5	BU402438 BU402438
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20	341.6	30.8	551	7	CO596606 CO596606
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23	336.8	30.3	761	7	CN078301 CN078301
24	331.8	29.9	533	7	CO612657 CO612657

c	25	329.2	29.7	532	7	CO611691	CO611691 DG9-107b5
c	26	317.6	28.6	600	4	BG807626	BG807626 2064-06 M
c	27	315.8	28.5	533	7	CO658472	CO658472 DG34-20c3
c	28	303.4	27.3	969	6	CD242494	CD242494 AGENCOURT
c	29	303	27.3	529	5	BU251898	BU251898 603404337
c	30	299.4	27.0	1073	5	BU131941	BU131941 603117709
c	31	297.8	26.8	722	4	BG722248	BG722248 602695456
c	32	293.4	26.4	683	6	BY703616	BY703616 BY703616
c	33	292.2	26.3	579	5	BU407817	BU407817 603483546
c	34	284.6	25.6	455	7	CO600294	CO600294 DG8-1c24
c	35	280.6	25.3	602	4	BG246890	BG246890 602360986
c	36	266.8	24.0	762	5	BU384694	BU384694 603858418
c	37	266	24.0	855	6	CD362407	CD362407 AGENCOURT
c	38	259.8	23.4	569	5	BX926432	BX926432 BX926432
c	39	244.2	22.0	679	7	CN078302	CN078302 EC2BBA14D
c	40	242	21.8	813	5	BU339658	BU339658 603514418
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c	43	218.4	19.7	735	6	CD100521	CD100521 AGENCOURT
c	44	211.2	19.0	478	7	CN481465	CN481465 hw08a07.Y
c	45	199	17.9	639	2	BB653271	BB653271 BB653271

ALIGNMENTS

RESULT 1
AF113216
LOCUS AF113216 3739 bp mRNA linear HTC 12-APR-2002
DEFINITION Homo sapiens MSTP036 mRNA, complete cds.
ACCESSION AF113216
VERSION AF113216.1 GI:11640579
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Liu, B., Liu, Y.Q., Wang, X.Y., Zhao, B., Sheng, H., Zhao, X.W., Liu, S.,
Xu, Y.Y., Ye, J., Song, L., Gao, Y., Zhang, C.L., Zhang, J., Wei, Y.J.,
Gao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y.,
Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.
Direct Submission
Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular
Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,
Beijing 100037, P.R. China
Location/Qualifiers
1. 3739
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YSVNIIRREKIANVFPFRCILIVRCGRCNCCGTYNMSCTCNSKTYKTHVLOFE
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FEATURES

ORIGIN
Query Match 71.9%; Score 798; DB 3; Length 3739;
Best Local Similarity 56.4%; Pred. No. 2,1e-190;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAGMGNYNATHTTGNTAVACNTNATHTGNGCNAATVYGYNSMTGNGAY 60
DB 107 ATGCAGCGGTCATCTTGTCTACACTCTAATCTCGCAACTTTCAGACGTGCGGAC 166

Qy	61	ACNMSNCNACNCCNARMSGCMWSNAATHAARCNVTNMGNAAYGCNAAYTNMGMN	120
Db	167	ACTTCTGCACCCCGAGGCGCATCTCAAACTTTGGCAACGGCAACTCGAGCGCA	226
Qy	121	GAYGARNNAAYCAAYTNACNGAYTNTATAYMGNGNAGAYARACNATHCARGTNNAARGN	180
Db	227	GATGAGAGCAATCACTCAAGACTTGTACCAAGATAGAGACNATCCAGGTGAAGA	286
Qy	181	AATGNGAYATNCNARMSNCCMGTTCYCNAAIWSNTAYCCMNGMAAYTNVTNTYNACN	240
Db	287	AACGGCTACGTGACAGAGTCTTAAGATTCGCAACAGCTAACCCAGAAACCTGCTCGACA	346
Qy	241	TGGMNTYNTCAVYMSNCARGARAAAYACMNGNATHCARVTNGTNTTYGAYACRTTYGNG	300
Db	347	TGCGGGCTTCACTCTCGAGGAATPACCGGATPACAGTATGTTTGACNATCGATTGGA	406
Qy	301	YTMGAARGCNGARAAAYGAYATHHTGYMNTAYGAYTYYGTNGARGTNGARGAYATHMSN	360
Db	407	YTMAGAGAACMAGMAAATGATATCTAGGTATGATTTGTGTGAMATGGAATGAAATATATCC	466
Qy	361	GARACMWSNACNATHATHTMGNGMNGTGTGTGSCNCAVBARARBTNCNCCMGNATH	420
Db	467	GAAACCAAGTACCATTTATYAGAGACATGTGTGTGACACAAAGAAAGTCTCCCAAGAA	526
Qy	421	AARMSMGNACNNAAYCARATHAARATHACNTTYAARWSNGAYATYATYYTGTNGCAAR	480
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Qy	481	CCNGGNTTYAARATHATYATYVMSNTYNTYNGARGATYTCARCCNGCNCNGMNSNGAR	540
Db	587	CCGTGATTCAGATTTATTTATTTCTTGTGGAAGATTTCCAAACCGCACACTTCACAG	646
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Db	647	ACCAACTGGGAATCTGTCAACAAGCTCTATTCAGGGGTATCTATACCTCTCATCAGTA	706
Qy	601	ACNGAYCCNAACNYTNA THGNCNAGCNYTNGAYAAARAAATGNCAGRTTYGAYACNGTN	660
Db	707	ACGGATCCCACTGTGATTCGGAGTGTCTGCGCAAAAATTTGCAAGAAATTTGATACAGTG	766
Qy	661	GARGAYTNTYNAARTAYTYYTAAYCCNGARMSNTGGCARGARAYYTNGARAAAYTGTAY	720
Db	767	GAAGATCTGCTCAAGTACTTCAATCCAGAGTCAATGCGCAAGAAAGATCTTGAGAAATGTAT	826
Qy	721	YTMNGAYACNCMNGNTAYWNGNGMNGMNSNTAYCAV GAYMGNAAARMSNARGTNGAYTN	780
Db	827	CTGGACACCCCTCGGTATCTGAGGCGAGCTATCCATGACCGGAAATTCAAAGTTGACCTG	886
Qy	781	GAYMGNNTYNAAYGAYGAYGCNAAARMGNTAYMSNTGAYACNCCMNGMAATYATWSNCTNAY	840
Db	887	GATAGGCTCAATGATGATGCCAAGGTTACAGTTGCACTCCAGAGAAATTACTCGGTCAAT	946
Qy	841	ATHMNGARGARYYNAAYTNGCNAAVGTNGTNTTYTCNMGNTGYTYNTNGTNCAR	900
Db	947	ATPAAGAGAGAGCTGAGATGGCCAAATGTGCTCTTTCACAGTTGCTCCTCGTGAG	1006
Qy	901	MGNTYGGNNGNAAATGYGNGTGYGSCNACNGTNAYTSGMNGMNSTYGAACNTGYAAVMSN	960
Db	1007	CGCTGTGAGGAAATTTGGCTGTGGAACGTGTCAATCGAGAGTCTCTGACATGCAATTTCA	1066
Qy	961	GGNAAACNGTNAAPARTAYCAVGARGTNTNCARTTYGARCCNGGNCAYATAPARMGN	1020
Db	1067	GGGAAAAACGTGAAAAAATATCATGAGGTATTAACAGTTTGAGCCGTGGCAATCAAGAG	1126
Qy	1021	MGNGMNGNCGNAAARACNATGGCNYTNGTNTNCAVATHCARVTNNGAYCAVCAVGAPMGNTGY	1080
Db	1127	AGGGGTAGCTTAAGACCATGCTCTTAATTGACATTCAGTTGATTCACATGAACGATGT	1186
Qy	1081	GAYTGYATHTGYWSMNSMNGCNCNMNG 1109	
Db	1187	GATTTGATCTGCAGCTCAAGACCACTCTCG 1215	

RESULT 2	AY419997	1095 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	AY419997				
DEFINITION	Homo sapiens HCM7077 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY419997.1 GI:39775954				
VERSION	GSS.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Primates; Nates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1095) Clark,A.G., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Feriencia,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trics				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1095) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Feriencia,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
AUTHORS	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them based on alignment.				
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ORIGIN					
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Matches 617;	Conservealtive 294; Mismatches 180; Indels 18; Gaps 1;				
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1	ATGACCGGCTCATCTTGTCTACACTCTAATCTTGGCAAACTTTTGCACTGTGGAC 60				
61	ACMWSNGCNAACNCNCARMSNGCNSNATHAARGCNYTMNGNAAYCNAAYTTMNGM 120				
61	ACTTCTGCAACCCCGCAGACGCGATCCATCAAGCTTTGGGCAACGCCAACCTCAAGCG 120				
121	GAYGARSNAAYCAAYTTNACNGAYVYNTTVMGMNGAGAGAPACNATHCARGTNAARG 180				
121	GAT-----GACTTGATCCGAAGAGAGACCACTCAAGCTGGAAGA 162				
181	AAYGNTAYGTNCARMSNCNMNTTCCNAAYWSNTATVCMMNGNAAYTNTNTNACN 240				
163	AAGCGTACGTGAGAGATCTAGATTTCCGGAACAGTACCCACAGAACTGCTCTGACA 222				
241	TGGMGVNTNAYVNSNCARGARAAVYACMGNATHCARVYTNNTTGYAAYCAATTYG 300				
223	TGGCGGCTTCACTCTAGAGAAATACACGAATACAGCTAGTGTTCGACATCAGTTTGA 282				
301	YTNAGARGCNCARAAAYGATVTHGYMNTAYGAYTTGTGARGTNGARGAYATHTSN 360				
283	TTAGAGAGACGAAGAAATATATCTGTAGATATGATTTTGTGAAGTTGAAATATATCC 342				
361	GAPACWSNACNATHTHNGCNGMNGTGTGYGNCAYAAARGATNCCNMGNATH 420				
343	GAACACAGTACATTAATTAGAGAGATGATGTGACACAAAGAGATTCCTCAAGAT 402				

Oy		421	AABSMNMACNAAACAATTAARATHAANTTYAARMNGAYATYATVYTGTNCNAR	480
Db		403	AAATCAAGAACGAACCAAATTAAATCAACATTCAAGTCGGATCTACTTGTGGCTAAA	462
Oy		481	CCGNGNTYYAARAATHTAATAWNSNTNYTNNGARGAYTYTCARCNGCNGCNCSNGAR	540
Db		463	CCTGAGATTCAAGATTATTTATCTTGCTCGAAGAATTTCCAAACCCGCAGCACTTCAAG	522
Oy		541	ACNAAYTGGGARWSNGTNA.CMNSMSNSAITHMSNGNGTMSNTAYAAYWSCNMSNGTN	600
Db		523	ACCAACTGGGAATCTGTCAACAAGCTCTATTTCAAGGGGTATCCTATACTCTCACAGTA	582
Oy		601	ACNAGYA.CCNACMYTHA.THCNGNAYGCNTYNGAYARARAETHGNCAGTTYAYACNGTN	660
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Oy		901	MGNTGYGNGNAA.YTGYGNTGYGANA.CNGTNAAYTSGMGNMSNTGYACNTGYAA.YWSN	960
Db		883	CGCTGTGAGGAAATTTGTGGCTGTGGAACGTGC.CAATGCACTGGAAGGTCCTGCACATGCA	942
Oy		961	GSNA.RACNRTNAAABAATYACAYARGNTYNTCA.PTYTGARCCNGCNCA.YTHAARMGN	1022
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Oy		1081	GAYTGATHTGY.MSNMSNMGN.CNCCNNMG	1109
Db		1063	GATTSTATCTG.CAGCTCAAGACCACCTCG	1091
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DEFINITION	Pan troglodytes HCM077 gene, VIRTUAL TRANSCRIPT, partial sequence.			
ACCESSION	AY419998			
VERSION	AY419998.1 GI:3975955			
KEYWORDS	GSS.			
SOURCE	Pan troglodytes (chimpanzee)			
ORGANISM	Pan troglodytes			
REFERENCE	Mammalia; Mollusca; Chordata; Craniata; Vertebrate; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan. 1 (bases 1 to 1095) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smirsky,J.J., Adams,M.D. and Cargill,M. Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios			
TITLE	Science 302 (5652), 1960-1963 (2003)			
JOURNAL	14671302			
PUBMED	2 (bases 1 to 1095)			
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,			
AUTHORS				

TITLE										Perrieria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.									
JOURNAL										Submitted (16-NOV-2003) Celera Genomics, 45 West Gate Drive, Rockville, MD 20850, USA									
COMMENT										This sequence is made by sequencing genomic exons and ordering them based on alignment.									
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ORIGIN																			
Query Match										68.2%; Score 756.8; DB 9; Length 1095;									
Best Local Similarity										55.7%; Pred. No. 2,6e-180;									
Matches										618; Conservative 293; Mismatches 180; Indels 18; Gaps 1									
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DB	61	ACTCTGCAACTCCGACGGCCAT	CCATCAAAAGCTTGGCGAAGCCCAACTCGGCGCA	120															
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DB	121	GAT-----	GACTTGTRCCGAAGAGTGAACCACTTCAGGTGA	162															
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QY	661	GARGAYTNTYNTAA	TATTTTAAATTAATTAATTAATTAATTAATTAAT	TATTTTAAATTAATTAATTAATTAATTAATTAAT	720	661	GARGAYTNTYNTAA	TATTTTAAATTAATTAATTAATTAATTAATTAAT	720										
DB	661	GARGAYTNTYNTAA	TATTTTAAATTAATTAATTAATTAATTAATTAAT	720															
QY	721	YTNAGVCCNAC	NYTNATHG	CNGAYVCNTYNGAYV	AAARATHG	780	721	YTNAGVCCNAC	NYTNATHG	CNGAYVCNTYNGAYV	780								
DB	721	YTNAGVCCNAC	NYTNATHG	CNGAYVCNTYNGAYV	AAARATHG	780													
QY	781	GAAYGATCTG	CACTTCACTTCACTTCACTTCACTTCACTT	CACTTCACTTCACTTCACTTCACTTCACTT	840	781	GAAYGATCTG	CACTTCACTTCACTTCACTTCACTTCACTT	840										
DB	781	GAAYGATCTG	CACTTCACTTCACTTCACTTCACTTCACTT	840															

Db		763	GATAGGCTCAATATGATATGCCAAGCGTTACAGTTCACGTCCACGGAAATTACTGGCATC	822
Qy		841	ATTMGNGARGARTTAARATYMGCAAAYGTNGINTVITTYVCNNMNTGYTTYNTNGTCAR	900
Db		823	ATAAGGAAGAAGCTGGAAGTTGGCCAATGTGTCTCTTTCACGTTGCCTCCCTCGTGAC	882
Qy		901	MGNTGVGSNGNNAAYGYGGANTGYGGNACNGTNAATYTGGMGNMSNTGYACNTGYA	960
Db		883	CGCTGTGAGAGAAATTTGTGCTGTGCATCTGTAACTGGAGGGTCTGGCACATGCAATTCA	942
Qy		961	GGAAAAACCGTGAAGAAAGTATCATGAGGTATTACA GTTTGA GCGCTGGCCACATCAAGAG	1002
Db		1021	MGGGAMGNGCNAAABACNAATGCGNTMNTGNAATHTCAATYTNGATYATYACGAR	1082
Qy		1003	AGGGGTAGAGCTTAGACCAATGGCTGTAGTTGACATCCAGTGGATCAACATGAAGATGC	1062
Db		1081	GAYTGYATHPTGYVMNSNMNGNCNCMMG	1109
Qy		1063	GATTGTATCTGCGAGCTCAAGACCACTCG	1091
RESULT 4				
AK003359				
LOCUS		1797 bp	mRNA	linear HTC 03-APR-2004
DEFINITION			Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D mRNA, full insert sequence.	
ACCESSION		AK003359		
VERSION		AK003359.2 GI:26382601		
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE				
AUTHORS		1	Carninci,P. and Hayashizaki,Y.	
TITLE			High-efficiency full-length cDNA cloning	
JOURNAL			Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE			99279253	
PUBMED			10349636	
REFERENCE		2		
AUTHORS			Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komoto,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
TITLE			Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL			Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE			20499374	
PUBMED			11042159	
REFERENCE		3		
AUTHORS			Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,U., Nishi,K., Kitamura,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Irawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawal,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.	
TITLE			RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL			Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE			20530913	
PUBMED			11076861	
REFERENCE		4		
AUTHORS			The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
TITLE			Functional annotation of a full-length mouse cDNA collection	
JOURNAL			Nature 409, 685-690 (2001)	
MEDLINE			5	
PUBMED				
REFERENCE				
AUTHORS			The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE			Analysis of the mouse transcriptome based on functional annotation	

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 SOURCE
 CDS
 ORIGIN

60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1797)
 Adachi,T., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
 Arakawa,T., Bono,H., Caraminci,P., Fukuda,S., Fukunishi,Y.,
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
 Hirooka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Iwata,M.,
 Kasubawa,T., Kato,H., Kawai,Y., Kojima,Y., Komono,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nihei,K.,
 Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
 Saeto,H., Saito,R., Sakai,K., Sakai,K., Sano,H., Sasaki,D.,
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
 Tezuka,H., Tagami,M., Tagawa,A., Takanashi,F., Tanaka,T.,
 Tejima,Y., Toya,T., Yamamura,T., Yashinishi,A., Yoshida,K.,
 Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
 Kanagawa 230-0045, Japan (E-mail:genome-resgsc@riken.jp,
 URL:ftp://genome-gsc.riken.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 On Dec 10, 2002 this sequence version replaced gi:12833975.
 Please visit our web site (http://genome-gsc.riken.jp/) for further
 details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5'-GAGAGAGAGAGCGCGCGCAACTGACATCTTTTCTTTTCTTTTAA 3'], cDNA was
 prepared by using trehalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. Second
 strand cDNA was prepared with the primer adapter of sequence[5'-
 GAGAGAGAGAGATCCAGACGACGCAATTAATTAATTAACCCCCCCC 3']. cDNA was
 cleaved with XhoI and SctI. Cloning sites, 5' end: SctI; 3' end:
 XhoI. Host: SOLR.
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 /mol_type="mRNA"
 /strain="C57BL/6J"
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 /db_xref="taxon:10090"
 /clone="1110003109"
 /issue_type="whole body"
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 /dev_stage="18-day embryo"
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 HTLVDYRENIQVTSNGHVSPPFPNSYPRNLLTWMLSQEKTALQLSFDQFGLAE
 EARNIDICRDFVEQPEASSTWSSGCHKEIPRITRTNOKITPSSDVFYFAK
 PGKFIYSPFEDFQPEASSTWSSGCHKEIPRITRTNOKITPSSDVFYFAK
 TVELDKHNPVSMODILENTLYIDTPHYRARSVHDRSKYDRLRINDVRYSTPKN
 HSNVLRBELTLNVAVPPRCLLYQRCGANGCGCTVPAK"
 PGHFKRGRKAKNALVDIQDHRERCDCISSRPP"

64.4%; Score 714.8; DB 3; Length 1797;
 Best Local Similarity 52.5%; Pred. No. 1,7e-169;
 Matches 582; Conservative 289; Mismatches 238; Indels 0; Gaps 0;

1 ATGCAWGNNTNATHTTGTGNTVACNNTNATHTGVCNNAAYTTTGTGWSNTGWMNGAY 60
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 186 ATGCAACGGCTCGCTTAACTCTCATCTCTCTCTGCGCGAATTGAGCTCTTATCGCGAC 245
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QY 61 ACGNSNGCNAACCCGACGAGAGAGATCAATCAAGCTTTGGCGAATGCCAATCCCTCAGGAGA 120
Db 246 ACTTTGGAGCTCCGACGAGAGATCAATCAAGCTTTGGCGAATGCCAATCCCTCAGGAGA 305
QY 121 GAYGARSNAAYCAAYTTNACGAYTTNTAYMGNGNGAYGARAACNATHCAGTNAARAGN 180
Db 306 GATGAGACCAATCACTCAGAGACTTGTATCCAGAGAGAGAGAAATTCAGGTGACAAGC 365
QY 181 AAYGNTAYGTNCARMSNCCNMGNTTYCCNAAYSNNTAYCCMGNAAAYTNTYNTACN 240
Db 366 AATGCCCATGTGCAAGAGCTCTGCTCCGGAACACTCCCAAGAGAACCTGCTTCGACA 425
QY 241 TGGMGNTNCAVMSACGARAAYACNMGNATHCARNTNGNTTYGAAVACARTTYGAGN 300
Db 426 TGGTGGCTCCGTTCCAGAGAGAAACAGGATACACTGCTCTTGACATCAATTCGGA 485
QY 301 YTNAGARGAGCGAARAAVAYHTGYMNTAYGAYTTTGTNGARGTNGARGAYATHMSN 360
Db 486 CTAGAGGAGAGCAAAATGACATTTGTAGATGACTTTGTGGAGTTGAAGAACTCTCA 545
QY 361 GARACNSNACNATHATHTMGNGNGNTGTGTGNCAYAARAGATNCCNMGNATH 420
Db 546 GAGAGCAGCACTGTGTGAGAGAGATGTGTGCGCAAGAGAGATCCCTCAAGAGATA 605
QY 421 AARSMNMGNAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Db 606 ACGTCAAAACAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 665
QY 481 CCNGNTTYAARATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Db 666 CTTGATTTCAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 725
QY 541 ACNAAATGGARWSNNTNACNWSNNSNATHTMSNGNTNWSNTAYAAVWSNCCNMSGNTN 600
Db 726 ACCAACTGGAGATCAGTCAAGACTCTTCTCTGGGGTGTCTCTATCACTCTCATCAATA 785
QY 601 ACNAAACNACNNTNATHGNCAYGNCYNTNGAYARABATHTGNCARTTYGAYACNNTN 660
Db 786 ACGGACCCCACTCTCAGTGTGATGCTCCGACAAACCTGCGAGAAATTCATATCCGCTG 845
QY 661 GARGAAYTNTNAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 846 GAAGATCTACTTAAGCACTTCAATTCAGTGTCTTGGCAAGATGACTGAGAAATTTGAT 905
QY 721 YTNAGACNCCNMGTAYMGNGNWSNNTAYCAVAYMGNAAFMSNAAAGTNGAYTTN 780
Db 906 CTGGACACCCCTCATTTATAGAGGAGCTCATTCATGATCGGAAGTCCAAAGTGAGACTG 965
QY 781 GAYMGNTNAAVGAAGACNAAABMGNTAYMSNTGYACNCCMGNAAATTAVMSNCTNAY 840
Db 966 GACAGGCTCAATGATGATCAAGGCTTACAGTTCACCTCCAGAAATCACTCTGTGAAC 1025
QY 841 ATTHMGNGARGAYTNAAYTNGCNAAYTNGTNTTYTTCNMGNTGYTYTNTYNTNGAR 900
Db 1026 CTCAGGAGAGAGCTAAGCTACCAATGCAAGCTTCTTCCACGATGCTCTCTGCGAG 1085
QY 901 MGNTGYGNGNAAVYGTGNTGYGNAACNGTNAAYTGGMGNSNTGYACNTGYAAVYSN 960
Db 1086 CGCTGTGTGCAACTGTGTGTGCGGAACGTGCACTGGAAGTCTCTGCAATGACAGCTCA 1145
QY 961 GGNABACNNTNAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Db 1146 GGGAAAGACAGTGAAAGATATATAGATTTGAAGCTTGGACCTGAGCAATTTCAAGAGA 1205
QY 1021 MGNMGNGNCGAARACNATGCGNTNGTNGAYATHCARNTYNGAYCAVAGABMGNTGY 1080
Db 1206 AGGGCAAGCAATCAAGATATATGCTTGTGTGATATCCAGCTGATCATATAGAGATGT 1265
QY 1081 GAYTGYATHTGYWSNWSNCCNCCNMNG 1109
Db 1266 GACTGTATCTGACGCTCAAGACCACTCG 1294

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RESULT 5
AY419999
LOCUS AY419999 1095 bp DNA linear GSS 12-DEC-2003
DEFINITION Mus musculus HCM7077 gene, VIRUTAL TRANSCRIPT, partial sequence.
ACCESSION AY419999
VERSION AY419999.1 GI:39775956
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1095)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tenenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence is made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
source
location/Qualifiers
1..1095
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/db_xref="taxon:10090"
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/locus_tag="HCM7077"
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Best Local Similarity 51.7%; Pred. No. 2,4e-159;
Matches 573; Conservative 283; Mismatches 235; Indels 18; Gaps 1;
QY 1 ATGCAACGCGCTCGTTTGTAGTCTCCATCTCCTGTGCGGAACCTTGAAGCTGATCCGAGC 60
Db 1 ATGCAACGCGCTCGTTTGTAGTCTCCATCTCCTGTGCGGAACCTTGAAGCTGATCCGAGC 60
QY 61 ACGNSNGCNAACCCGACGAGAGAGATCAATCAAGCTTTGGCGAATGCCAATCCCTCAGGAGA 120
Db 61 ACTTTGGAGCTCCGACGAGAGATCAATCAAGCTTTGGCGAATGCCAATCCCTCAGGAGA 120
QY 121 GAYGARSNAAYCAAYTTNACGAYTTNTAYMGNGNGAYGARAACNATHCAGTNAARAGN 180
Db 121 GAT-----GACTTGTACAGAGAGAGAGAAATTCAGGTGACAAGC 162
QY 181 AAYGNTAYGTNCARMSNCCNMGNTTYCCNAAYSNNTAYCCMGNAAAYTNTYNTACN 240
Db 181 AATGCCCATGTGCAAGAGCTCTGCTCCGGAACACTCCCAAGAGAACCTGCTTCGACA 222
QY 241 TGGMGNTNCAVMSACGARAAYACNMGNATHCARNTNGNTTYGAAVACARTTYGAGN 300
Db 241 TGGTGGCTCCGTTCCAGAGAGAAACAGGATACACTGCTCTTGACATCAATTCGGA 282
QY 301 YTNAGARGAGCGAARAAVAYHTGYMNTAYGAYTTTGTNGARGTNGARGAYATHMSN 360
Db 301 CTAGAGGAGAGCAAAATGACATTTGTAGATGACTTTGTGGAGTTGAAGAACTCTCA 342
QY 361 GARACNSNACNATHATHTMGNGNGNTGTGTGNCAYAARAGATNCCNMGNATH 420
Db 361 GAGAGCAGCACTGTGTGAGAGAGATGTGTGCGCAAGAGAGATCCCTCAAGAGATA 402

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QY 832 MSNGTAAATTHMGNGARGARYTNAARYTNGCNAAVGTNGTNTTYYTTCNMNGNTGYTN 891
 DB 588 TCTGCAATTTAAGGAAGAACTGAAGTGAACAAATGCTGTTCTCTCCCTGCTGCC 657
 QY 892 YTNGTNCARMGNTGYGNGGNAAYTGYGNTGYGNAAGTGAATYTGGMGMSNTGYACN 951
 DB 658 CTGTGCGAGCGCTGTGAGGAAATTTGTGGCTGTGAACTTCAATGGGAAATCTCGACG 717
 QY 952 TGYAATWSNGGNAACGCTNAARATRYCAYGARGTNTYTCATTGACGCG 1006
 DB 718 TGCATGTCCGGGAAAAAGTGAACAAATATCATGTAGGTCTGAAATTTGTCGCCG 772

RESULT 7
 BE914552 799 bp mRNA linear EST 29-SEP-2000
 LOCUS 60165653p1 NC1_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3965677 5',
 DEFINITION mRNA sequence.
 BE914552
 ACCESSION BE914552.1 GI:10413295
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 799)
 NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgarphb@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 http://image.llnl.gov
 found through the I.M.A.G.E. Consortium/LMLN at:
 Plate: LMLN9137 row: j column: 14
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 Location/Qualifiers
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 /clone="IMAGE:3965677"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="3 months, virgin"
 /lab_host="DH10B"
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 /note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN
 Query Match 41.4%; Score 459; DB 2; Length 799;
 Best Local Similarity 50.1%; Pred. No. 8.3e-105;
 Matches 400; Conservative 207; Mismatches 185; Indels 6; Gaps 2;

QY 111 YTTTNGMNGNGAYGARGMSNAAYTNAACGAYTTTATYMGNGNGAYGARGACATCA 170
 DB 1 CCTCAGGAGATGAGCAATCACCTCACGACTTGAACGAGAGAGAGAAACATTC 60
 QY 171 RGTNAAAGGNAAYGNTAYGTNCARMSNCNMNGTTCNNAAVMTNTAYCCMNGNAAYT 230
 DB 61 GGTGCAAGCAAGGCGCATGTGCAAGTCTCTGCTCCGAAACACTACCAAGAACT 120
 QY 231 NYTNTNACNTGCMGNTYTCAYMSNCARGARAAYACMNGNATHCARYTNTGTYGAY 290
 DB 121 GCTTCTGACATGTGTGCTCCGTTCCAGAGAAAAACGGAATPACAATGCTCTG 180

QY 291 YCAFTTGGYNTNGARGCGNGARAYGAYATHTGTMGNTAYGATYTYTGNGARGTNGA 350
 DB 181 TCAATTCGACCTAGGAGAAAGCAAGAAATGACATTTGTAGTATGACTTTGTGAAGTTGA 240
 QY 351 RGAATWSNGARACMWSNACNATATHTMGNGMNGTGTGTGNGCAVYARGAGTNGC 410
 DB 241 AGAATCTCAGAGACACACACTGTGTGAGGAAAGATGTGTGCGCAACAGAACTCCC 300
 QY 411 NCCMNGNATHAARMSMNGACNAAYCAPATHAARATHTACNTTYAARMSNGAYATATT 470
 DB 301 TCCAAGATTAACGTCAAGAACAAACCAATTAATTAATCAATTTAAGTCTGATGACTACTT 360
 QY 471 YGTNGCNARCCNGGNTTYAARATHTATATYATVANSYNTNTNGARGATYTYCARCNGCNGC 530
 DB 361 TGTGCAAAACCTGATTCAGATTTATTTATTCATTTGTGAGAAATTCACACCGGAAGC 420
 QY 531 NCCMNSNGARACNAAYTGGARWSNGTNAACMWSNATHMSNGNGTMSNTAYAAVWS 590
 DB 421 AGCCTCAGAGACCAACTGGAATCAGTCAAGCTCTTCTCTGTGGGGTGTCTTATCAGCTC 480
 QY 591 NCCMNSNGTNAACNAYCCNACNTYNTATGCGNAYCCTTNGAYAAPARATHTGNGARTT 650
 DB 481 TCCATCAATTAACGAGACCCCACTCTCAGTCTGATGCCCTGGAACAAACCTGTGCGAGATT 540
 QY 651 YGAYACNGTNGARGAYTNTYNTAARTATYTYAAYCNGARGMSNTGCGARGAYYTNGA 710
 DB 541 CGATACCGTGGAGAGTCTACTTAAGCACTTCAATCAATGCTTTGGCAAGATGATCTGGA 600
 QY 711 RAAVATGTAAYTNGAYVACNCCNMGTAYMGNGMNSNTAYCAYGAYMNAARWSNA 770
 DB 601 GAATGATGATCTGCAACACCCCTCATTATAGAGGACAGTGCATCATGATCGGAATGCCA 660
 QY 771 RGTNCAVYTNAMGNTYNTAAYGAYGAYGCAARMGNTAYMSNTGYACNCCMNGAAATYA 830
 DB 661 AGTGAGGTGCGACAGCTCAATGATGATGATCAAGTCAAGTTCCTCCCGAGATCAC 720
 QY 831 YMSNGTNAAYTTHMGNGARGARYTNAARYTNGCNAAVGTNGTNTTYYTTCNMNGNTGYT 890
 DB 721 TCTCTGGAAC--TCGAGAGAGCTGAACT---GAACATGGAGTTCCTCGACGATGGCT 774
 QY 891 NYTNGTNCARMGNTGYG 908
 DB 775 CCTCTGCAAGCTGGCTG 792

RESULT 8
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 LOCUS 603106994p1 CSEQCHN04 Gallus gallus cDNA clone CHEST47124 5', mRNA
 DEFINITION sequence.
 BU213231
 ACCESSION BU213231.1 GI:25387621
 VERSION
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1044)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Boech, B.,
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.U.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 12445392
 CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1OD, UK
 Tel: 01612008930
 Fax: 01612360409

FEATURES
source

Email: Simon.Hubbard@unist.ac.uk.

Location/Qualifiers

1..1044

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hixex"

/db_xref="taxon:9031"

/clone="CHEST47124"

/issue_type="whole embryo"

/dev_stage="20-21"

/lab_host="DH10B"

/clone_1lb="CSBQCHN04"

/note="Organ: whole embryo; Vector: pBluescript II KS(+);

Site 1: EcoRI; Site 2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methyalted C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was bluntended, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

ORIGIN

Query Match 40.8%; Score 453; DB 5; Length 1044;

Best Local Similarity 50.2%; Pred. No. 3.3e-103;

Matches 413; Conservative 212; Mismatches 189; Indels 8; Gaps 4;

QY 100 MGNAAAGCAATYTTGNGMNGAYGARMNAAYCAVYTAACGAYTTATYVNGMNGAY 159
 DB 14 AGTAAGAGAGTTCAAGAGTTGTTTACAGCAATCACTTCACTTCACTTCACTTCA 73
 QY 160 GABACATATCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 219
 DB 74 GAGACCATAGTGGCGAGGAATGCTGCATCCACAGCTCTCGCTCCGAGCAGTTAC 133
 QY 220 CCNMGAAAYTTATYTTATCACTGAGTTCATCACTGAGTTCATCACTGAGTTCAT 279
 DB 134 CCCAGAACTCTCTCTGACATGCGGCTGCGCTCCCGAGAGACCAAGATTCAGCTG 193
 QY 280 GTTATYGAATCACTTGTGAGTTCATCACTGAGTTCATCACTGAGTTCATCACT 339
 DB 194 GCTTTGATATCACTTGTGAGTTCATCACTGAGTTCATCACTGAGTTCATCACT 253
 QY 340 GTNGAGTNGAGATATMSNGARACMSNACNATATHTMGNGMNGTGTGTGNCAY 399
 DB 254 GTGGAAGTGAAGATTATCAAGACCAAGATTAATACAGAGAAAGTGTGTGTGAC 313
 QY 400 AARGAGTNCNCCNMGNAATTAARMSNMGNAATTAARMSNMGNAATTAARMSN 459
 DB 314 AAGGAAGTACCTCCAAAGATTAATCAAGAAATTAATCAAGAAATTAATCAAG 373
 QY 460 GAYGATYTTATYTTATCACTGAGTTCATCACTGAGTTCATCACTGAGTTCAT 519
 DB 374 GATGATCTTGTGAGTTCATCACTGAGTTCATCACTGAGTTCATCACTGAGTTC 433
 QY 520 CARCCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 579
 DB 434 CAGC---ATGACAGCTCAAGAACTGAGAACTGAGAACTGAGAACTGAGAACTG 490
 QY 580 WSNATYAAWNSNCCNWSNNGTNAACNATYTAATHTMGNGMNGTGTGTGNCAY 639
 DB 491 TCCATCTCTCTCATCATGACCGACCTTCACTCAAGAGAAAGCTGTGAGTTC 550
 QY 640 ATGCGATYTTATYTTATCACTGAGTTCATCACTGAGTTCATCACTGAGTTCAT 699
 DB 551 ATTCTGATTCATCACTGAGTTCATCACTGAGTTCATCACTGAGTTCATCACTG 610
 QY 700 GARGAYTTNGARAAATGATYTTNGAYA---CNCNMGNTATYMGNGMNGTNAATY 756

DB 611 GAAATCTTCGAAATTTGTATACAGAAAGTGCCACCATTTTCAGAGACGATACAT 670
 QY 757 GAYMNAARMSNAAGTNGATYTTATCACTGAGTTCATCACTGAGTTCATCACT 816
 DB 671 GACAGAAAGTCCAAAGTTCATCACTGAGTTCATCACTGAGTTCATCACTGAG 730
 QY 817 ACNCCNMGNAATY---AYWNGTNAAYATHTMGNGMNGTGTGTGNCAY 875
 DB 731 ACTCGAGAAACTATCTGTCACTTATTAAGGAGAAAGTCAAGCTGACAAATGCT 790
 QY 876 YTTTCNMG-NTGYTTATYTTATCACTGAGTTCATCACTGAGTTCATCACT 916
 DB 791 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832

RESULT 9
 LOCUS BU326159
 DEFINITION BU326159 727 bp mRNA linear EST 28-NOV-2002
 603493350F1 CSBQCHN63 Gallus gallus cDNA clone CHEST399c13 5', mRNA
 sequence.
 ACCESSION BU326159
 VERSION BU326159.1 GI:25834160
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE
 AUTHORS Boardman, P.E., Sanz-Blanco, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Rong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken CDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomedical Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@unist.ac.uk.

FEATURES

source

Location/Qualifiers

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/organism="Gallus gallus"

/mol_type="mRNA"

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/db_xref="taxon:9031"

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/note="Organ: head; Vector: pBluescript II KS(+); Site 1:

EcoRI; Site 2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methyalted C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was bluntended, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

ORIGIN

Query Match 39.6%; Score 440; DB 5; Length 727;
 Best Local Similarity 52.1%; Pred. No. 5.2e-100;
 Matches 380; Conservative 189; Mismatches 155; Indels 6; Gaps 2;

Qy	221	CMGMAAAYTNVYTNVTAACGTGAGMNTYNCAYMSKACGARAAYACNGNATHCARVNG	280
Db	1	CCAGGAACCTCCTGTCGACATGCGCGCTGCACTCCCGAGAGCCACGAGATCCAGCTGG	60
Qy	281	TNTTGGVAAACARTTGGYNTNGARGARGCGNGARAAYATHTGVMGNTAYGAYTTTG	340
Db	61	CTTTGTGATTAATCAGTTTGGACTGAGAGAGCTGAAATATGATCTGCAAGTATGACTTTG	120
Qy	341	TNGARGTNGAAGAYATHTMSNGARACMSNACNAATATHTMGNGMNGNTGGTGGNCAY	400
Db	121	TGGAAGTGGAAAGATTATCAGAGACACACACGTTATACGAGAAAGTGGTGGGACACA	180
Qy	401	ARGAGTTCNCCNMNGNATTHAARMNMGNACNAACATATHAARATHTACNTTAYARMSNG	460
Db	181	AGGAAGTACCTCCAGAAATTAACATCAAGAACAAATCAAGTAAAGTAACTTCAAAATCCG	240
Qy	461	AYGAYTATYTTGTGNCNNAARCCNGGNTTAAATHTATATAYATVMSNTYNTNGARGAYTTG	520
Db	241	ATGACTACTTGTGTGCTAAACAGAGATTCAAGATTGTGTTACTCCTTGGATGATTTCC	300
Qy	521	ARCCNGCNGCNGCWSNNGARACNAAYTGGGARMSNGTNAACWSMNSNATHTMSNGGNTM	580
Db	301	AGC--ATGCAAGCCCTCAGAAAACCACTGGGAATCAGTCAAGACTCTGTCTCAGGGGTCT	357
Qy	581	SNTAYAAATSSCCNMNSNGTNACNGAYCCNAACNTYATGACNGAYGCNTNGAYAAABA	640
Db	358	CCTATCCCTCTTCATCACTAGTACCGACCTTCACTACACGACGAGAGCCCTGGATCAGACCA	417
Qy	641	THGCGARTTYGAYACNGTNGARGAYTNTYTAARTATYTAAYCCNGARMSNTGGCARG	700
Db	418	TTGCTGCATTTTGAACACTGTGGAAAGATCTGCTTAAACCTTAACTCAAGCTCCTGGAAAG	477
Qy	701	ARGAYTNTGARAAYATHTATYTTNGAY--CNCNMNGTAYMNGNGMNSNTAYCAVG	757
Db	478	AAGATCTCGAAGATTGTACACAGAAAGTGGCACATTTATCGAGGACGAGAACCTACATG	537
Qy	758	AYMGAAARMSNARGTNGAYYTNAGYVMGNTYTAAGAYGAYGCNAABMGNTAYMSNTGYA	817
Db	538	ACAGGAAGTCCAAAGTTGACCTCGACAGGCTGAATGATGTGAAGCGCTACACTGCA	597
Qy	818	CNCCNMGAAYATVMSNGTNAAYATHTMGNGARGARATYNAARTYNGCNAAYGTGNTTYYT	877
Db	598	CTCCAGAAACTACTCTGTCAATTAAAGGAAGACTGAAGCTGACAAATGCTGTTTTCT	657
Qy	878	TYCCMGNTGYTNTNTGTNCARMENTGYGNGGNAATTYGAGNTGYGNAACNGTNAAYT	937
Db	658	TCCCTCGCTGCTCCTCTGTTCACGCGCTGTGGAGAAATTTGGTGTGGAACCTTCAAAAT	717
Qy	938	GGMGMSNTG 947	
Db	718	GGAATCTCTG 727	
RESULT 10			
BUJ11960		985 bp	mRNA
LOCUS			linear
DEFINITION	60340553571 CSEQCHN61 Gallus gallus CDNA clone CHEST309e9 5', mRNA		EST 28-NOV-2002
ACCESSION	BUJ11960		
VERSION	BUJ11960.1		GI:25819961
KEYWORDS	EST.		
SOURCE	Gallus gallus (chicken)		
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
AUTHORS	Boardman,P.E., Sanz-Ezquerro,U., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.		
TITLE	A Comprehensive Collection of Chicken cDNAs		
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)		
MEDLINE	22335534		

[illegible]


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Db      481 GACACATTGTCGATTTGACACTGTGGAAGATCTGCTTAACACTTTAACTCCAGATCTCTG 540
QY      696 GCGARGAGAYTTNGARAAYTGTAYTTNGAYA---CNCNMGTAYMNGMNGMNSNTA 752
Db      541 GAAAGAGAGATCTGAGAAATTTGTACACAGAAAGTGCCACATTATCGAGGAGAGACTTA 600
QY      753 YCAYGAYMGAARWNSNARGTNGAYTTNGAYTMGNTNNAAYGAYGAGCAAAKMGNTAYMS 812
Db      601 CCAATGACAGAAATCTCAAGATGACCTGACAGGCTGAATGATGATGAACCGCTACAG 660
QY      813 NTGYACNCCMNGAAYTAYMNSGNTNNAAYTMHNGARGARYTNAAYTNGCNAAYTNGT 872
Db      661 -TGACATCCCAAGAAACTACTCTGTCAATTTAAGGGAAGAACTGAGCTACAATGCTTG 719
QY      873 NTYTTTCCMNGTGYTNTYNTGNCARGMGTGYGNGNNAAYTGYGNTGYGNACNGT 932
Db      720 TTTTCTCTCGCTGCTCTCTCTGTCCTGTCAGGCTGTGAGGAAATTTGCTGTGAAACTTC 779
QY      933 NAAVTGGMNWSNTGYACNTGYAAYMNSGNAABACNGTNAABARTYACAYGAGTNT 992
Db      780 AATTTGGAATC-TGACACTGCAATGTCGGGACACACCTGAACAATATC-TGACCTCTG 837
QY      993 NCARTTGYARCCNGGNCAYATTAARMNGMNGMNGMNGMNAARACNATGCGCNYTNGTGA 1052
Db      838 GAATTTGTCTCCGAGGCGGAGCATCCGAAAGAGCAAAAGCCAGAAATACTGTTAGT 897
QY      1053 YATHCARYTNGAYCAAYCAYGARMGNTG 1079
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RESULT 11
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LOCUS      603482511F1 CSEQCHN59 Gallus gallus cDNA clone CHEST372e3 5', mRNA
DEFINITION      BU0404150
ACCESSION      BU0404150
VERSION      BU0404150.1 GI:25773206
KEYWORDS      EST.
SOURCE      Gallus gallus (chicken)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
REFERENCE      1 (bases 1 to 798)
AUTHORS      Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
TITLE      Ford, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
JOURNAL      A Comprehensive Collection of Chicken cDNAs
MEDLINE      Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED      2235534
COMMENT      12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(MIUST)
PO Box 88, Manchester, M60 1OD, UK
Tel: 0161208930
Fax: 0161208930
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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FEATURES

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/organism="Gallus gallus"
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constructed from 1 million independent clones. cDNA"

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ORIGIN

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Query Match      38.5%; Score 427.4; DB 5; Length 798;
Best Local Similarity 51.5%; Pred. No. 8,76-97;
Matches 401; Conservative 198; Mismatches 170; Indels 9; Gaps 5;

QY      226 AAYTNTNTNACNTGCMGNTNCAAYWSCARGARAAYCNCMNATHCARYTNGTNTTY 285
Db      2 AACTCTGCTGACATGCGCGCTGCACTCCCAAGAGCAACAGATCCAGCTGCTTTT 61
QY      286 GAYAAACARTTGGNTNGARGARGCNGARAAYATHTGVMNTAYGAYTTTNGARG 345
Db      62 GATATCAATT-GGACTGAGAGAGCCGAAATGATTTCTGCAAGTATGATTTGGAA 120
QY      346 GTNGARAYATHTWSNGARACMSNACNATHTMNGMNGMNTGGTGYGNCAYARGAR 405
Db      121 GTGAGATATTTACAGACACACAGATATACAGAGAAAGTGTGTGGGCAAGAA 180
QY      406 GTNCCNCCMNGNATTHARMNGMNAACNAYCAATTAARATHCNTTYARMNSGAY 465
Db      181 GTACCTCGAAGATTAATCATCAAGAACATCAATTAAGTAACTTCAATCCGATGAC 240
QY      466 TAYTTGTGNCNARCCNGNTTYAARATHTAYTWSYNTYNTNGARGAYTTTCARCCN 525
Db      241 TACTTTGTGCTAAACAGAGATTCAGATTTGTTACTCCCTGTGATGATTTCCAGC-- 298
QY      526 GCGNGCMNSNARACNAAAYTGGGARMNGNTYACMSWSNATHTWSNGMNGMNSNTAY 585
Db      299 -ATGACGCTCGAAGAACCAACTGGGAATGATCAACAGCTCTGTCAGGGGCTCTAT 357
QY      586 AAYWSCNWSNGTNACNAYCCNATNTNATHGNGAYGVCYNTNGAYABARATHGNC 645
Db      358 CCTTCATCAAGTACGACCGACTTACATCAAGCAAGAGCCCTGATCAGACATTTGCT 417
QY      646 GATTYGAYACNGTNGARGAYTTNTAATYATYTTAAYCCNGARMSNTGGCARGARGY 705
Db      418 GCATTTGACACTGTGAGATGCTGCTTAAACATTTAATCCAGACTCTGGAAGAAAT 477
QY      706 YTMGARAAYATGTAYTTNGAYA---CNCNMGTAYMNGMNGMNSNTAYCAYGAYMGN 762
Db      478 CTGAGAAATTTGTACACAGAAAGTGCCACCACTTTCAGGAGCACTACATGACAG 537
QY      763 AARWSNARGTNGAYTTNGAYMNGNTNNAAYGAYGCAAAARMGTAYMSNTGYACN 822
Db      538 AAGTCCAAAGTTGACCTGAGAGGCTGAATGATGTAAGACCGCTACAGCTGACTCA 597
QY      823 MGNAAVTAYWSNGTNAAYTMHNGARGARYTNAARYTNGCNAAYTNGTNTTYTCN 882
Db      598 ACAAACACTCTGCTCAATTTAAGGAGAAACGAGAGCTGACAAATGCTGTTCTCCCT 657
QY      883 MGNATGYTNTNGT-NCARMGNTGYGNGNNAAYTYGSG-NTGYGNCNCGNTNAYTGM 940
Db      658 AGCTGCTCTCTGCTCCAGCGCTGTGAGGAATTTGCTGTGGAACCTTCAAAATTTGA 717
QY      941 GWSNTGYACNTGYAAYWSNNGNNAARACNGTNAABARTYACAYGAGTNTNCARTT 998
Db      718 GATCTTACGTGATGTGGGGGAAAAAACATGAAGAAATATCATGAGGTGCTGAATT 775

RESULT 12
BU015557      921 bp      mRNA      linear      EST 28-NOV-2002
LOCUS

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synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."


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/mol_type="mRNA"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

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ORIGIN

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Query Match      36.6%; Score 406.6; DB 4; Length 723;
Best Local Similarity 52.4%; Pred. No. 1.6e-91;
Matches 369; Conservative 161; Mismatches 150; Indels 4; Gaps 4;

278 TNGTNTTGAAYAAYCARTTYGNYTGARGGCGNCGAARAAGATATHTGNGMNTAAGAT 337
21 TGGGTTGACATCATATGCGGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 80
338 TTGTNGARGTNGARAGATATHTSNGAPACMSNACNAATHTATHTGNGG-NNGTGTGTG 396
81 TTGTGGAAGTTGAGAGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 140
397 CAAAGAGAGTNCNCGNMGNAATHTAHSNMGNACNAATCAATATATATATATATATAT 456
141 CAGAGAGAGATCCCTCCAGAGATACGATACAGAGAGAGAGAGAGAGAGAGAGAGAG 200
457 WSNAGATATATTTGTGNCNARCCNGNTTAAATATATATATATATATATATATATAT 516
201 TGTGATGACTACTTGTGGCAAAACCTGGATTCAGATTTATATATATATATATATAT 260
517 TTYCARCCGNCNCGNCGNMGNAACNAATYGGGAGSNGNACNWSNWSNATHTSNGN 576
261 TTCACACGAGAGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
577 GTNMTATATATATATATATATATATATATATATATATATATATATATATATATAT 636
321 GTGTCTATCACTCTCCATCAATATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
637 AARATHTGNGARTTYGATACNGTNGARAGATATATATATATATATATATATATATAT 696
381 ACTGTGAGAGATTCGATACCGTGTGAGAGATCTACTTAAAGCACTTCAATCCAGTCT 440
697 CARGARAGATATATATATATATATATATATATATATATATATATATATATATATAT 756
441 CAGATATATCTGAGAGATTTTATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
757 GATGAGAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 815
501 GATGAGAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560
816 YACNCGNMGNAATATATATATATATATATATATATATATATATATATATATATATAT 874
561 CACTGCCAGAGATCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
875 TTTTCCNMGNTATATATATATATATATATATATATATATATATATATATATATATAT 934
621 TCTTCCAGAGATCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 679
935 ATHTGAGAGATTCGATATATATATATATATATATATATATATATATATATATATAT 978
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RESULT 14
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LOCUS      811 bp      mRNA      linear      EST 28-Nov-2002
DEFINITION 603489249F1 CSECHN63 Gallus gallus clone CHEST388b13 5', mRNA
sequence.

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ACCESSION      BU326859
VERSION        BU326859.1
KEYWORDS       GI:25834860
SOURCE         EST
ORGANISM       Gallus gallus (chicken)
REFERENCE      Bukacynska, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
1 (bases 1 to 811)
AUTHORS        Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE          A Comprehensive Collection of Chicken CDNAs
JOURNAL        Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE        22335534
PUBMED        12445392
COMMENT        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

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FEATURES

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/notes="Organ: heads; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldi et al., Genome Research
(1996) 791, except that a significantly longer
reannealing hybridization was used."

```

ORIGIN

```

Query Match      34.6%; Score 384.6; DB 5; Length 811;
Best Local Similarity 49.6%; Pred. No. 6.5e-86;
Matches 397; Conservative 193; Mismatches 189; Indels 22; Gaps 6;

313 GARAAGATATATATATATATATATATATATATATATATATATATATATATATATAT 372
2 GAAAATGATATATATATATATATATATATATATATATATATATATATATATATATAT 61
373 ATHTATHTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
62 GTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
433 AATCATATATATATATATATATATATATATATATATATATATATATATATATATAT 492
122 AATCATATATATATATATATATATATATATATATATATATATATATATATATATAT 181
493 ATHTATATATATATATATATATATATATATATATATATATATATATATATATATAT 552
182 ATTTGTACTCTCTGTGATATATATATATATATATATATATATATATATATATATAT 238
553 WSNGTACNWSNWSNATHTSNGNMGNTATATATATATATATATATATATATATATATAT 612
239 TCAGTACAGAGATCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 298

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Qy	613	YTNATHGNGAGVGNVYTGAAVAARAPATHGNGARITTYGVAACNGTNGAAGAAVYTNNTN	672
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Qy	673	AARTAYTTTAAVCCNGARMSNTGGCARGARGAVYTNGARAAVATGTAVYTNGAVA--CN	729
Db	359	AAACACTTAATCCAGACTCCTCGAAGAAAGATTCGAGAAATTTGTACACAGAAAGTGAC	418
Qy	730	CCMNGNTAYMNGNGMGMWSTNATYCAVGAIMGNAAARMSNAARGTYNGAYTNNGAYNTN	789
Db	419	CACCAATTATCAGGACGAGAGCTACCATACAAGAAAGTTCMAAGTTGACCTGGACAGGCTG	478
Qy	790	AAVYGAYGCGNAARMGNTPAYMSNTGYACNCCMGNAAVYTAVMSNGTAAVATHMGNAR	849
Db	479	AATGATGATGTGAAGCCGCTACAGCTGCACCTCCAGAAACATCTCTGTCAATTTAAAGGAA	538
Qy	850	-GARTYNAARYTNGGNAAYVGTNGTJTYYYCCMNGNTGYTNTYNTGTCNARMGNTGYG	908
Db	539	CGAACTGAAGCTGACAAATGCTGTTTTCTTCCCTGGCTGCTCTTGTCCAGCGGTGG	598
Qy	909	NGGNAAYT-GYGGNTGYGNAACNGTNAAYTGGMGMSNTGYACNTGYAAVMSNGNAR	966
Db	599	AGGCAAAATTTGGGCTGTGGAACTTCAAAATTGGAATACTCGTGAAGTATGACCGGAA	658
Qy	967	ACNGTNAAR-AAATYCAVGARBNYNTCAATTYARCCNG-----GNCAYAT	1013
Db	659	ACAGTGAACCACTATCATGAGTGCTGAAAAATTTGTCCTCCCGAGCGGAGCATCCCCGAA	718
Qy	1014	HAARMGNNGNGMNGMNGCNABACNAATGCVNTGNTGNAAVATHCARNTNGAYCAVCAGA	1073
Db	719	CAGAAAGGCAAAAGCCAGAAAGAACATGAGCTTAGTAAGATYATACGTTGATCATCATGGA	778
Qy	1074	RMGNTGYAYTYGATHTGYMS	1094
Db	779	ACGTGGAGATGATCTGCAG	799

RESULT 15
 BU290871
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

BU290871 774 bp mRNA linear EST 27-NOV-2002
 603607294f1 CSEQCHN55 Gallus gallus cDNA clone CHEST519K24 5', mRNA
 sequence.
 BU290871
 BU290871.1 GI:25740327
 EST.
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 774)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392

Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1OD, UK
 Tel: 01612008930
 Fax: 01613360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
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location/qualifiers
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/clone_lib="cSEOCHN55"
/notes="Organ: kidney & adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 8228-8232 and Bonaldo et al., Genome Research
6 (1996): 791, except that a significantly longer
reannealing hybridization was used."

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Query Match	34.5%	Score 382.6	DB 5	Length 774
Best Local Similarity	50.6%	Pred. No. 2e-85		
Matches 346	Conservative 166	Mismatches 155	Indels 7	Gaps 2
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Db	1 ATTTATCAGAGACGACGAGTTATACGAGGAAGGTGTGGCCACAGGAATGACTCTC	60		
Qy	CMNQNATHAARMSMNGNACNAAVYCARATHAARHAACNTTYAARMSNGAVAYATRYTGY	472		
Db	61 CMAAATPACTACTCAAGAAACAATAGATPAAGATACCTTCMAATCCGATACATCACTTG	120		
Qy	TNGCNARCGNGNTTYAARATHATYAYMSNTYNTYNGARGATYTYCARCNCNGCNG	532		
Db	121 TGGCTAAACGAGATTCAGATTTGTACTCTCCCTTGGATGATTTCCAGATGACGCC	179		
Qy	CMNSNGARACNAAVYTGSGARWSNGTNA CMNSNWSNATHWSNGGTNWSNTAYAYMSNC	592		
Db	180 ---TAGAAACCAACTGGGAATCACTGTCACAGACTGTGCTCAGGGGTCTCTATCCCTCTC	236		
Qy	CMNSNGTNA CNAGVCCNAACNTYNA THGCNAGVGCNTYNGVYAAABAARATHGCNARPTYG	652		
Db	237 CATAGAGCCGACCCCTACACTCACACAGAAAGCCCTGGATCAACACATGTGCTCATTTG	296		
Qy	AYACNGTNGARGAYTYTYTNAARATYATYTYAACNCGARMSNTGCGARBARAYYNGARA	712		
Db	297 ACACTGTGGAAGATCTGTGTTAAACCTTAACTTCAGACTCCTGGAAAGAAATCTCGAGA	356		
Qy	AYATGTAYYTNNGAYV---CNCNMGNATAYMNGMGNMWSNTAYCAVGYMGNARMSNA	769		
Db	357 ATTTGTACACAGAAAGTGGCCACATTTATGAGGCAAGAGTACCATGACGAAAGTCA	416		
Qy	ARGTNGAYYTNNGAYMGTNTNAAYGAYGACNAAARMGTATWSTGTACNCCNMGNAAVT	829		
Db	417 AAGTTGACCTGSGACAGGCTGAATGATGATGGAAGGCCCTCACGCTGCATCCMAAAGAACT	476		
Qy	AYMSNGTNAAYATHMNGARGARATYNARLYTNNGNAAVYNTGNTTYTYCCNMGNXTY	889		
Db	477 ACTGTGTCATTTTAAAGGAAGAACTGGAAGCTGACPAATATGCTGTTTCTTCCCTGCTGCC	536		
Qy	TNTYNTGTCNARMGTGTGNGNGNAAVYTGAGNTYGGNACNGTNAAYTGGMNWSNTGYA	949		
Db	537 TCTTGTTCGACGCTGTGTGGAGAAATGTGTGCTGTGGAACCTTCAAAATTTGGAAATCTGCA	596		
Qy	CNTGYAAVWSNGNAAARACNGTNAARAATYACVARGTNYTNCARTTYGARCCNGNC	1009		
Db	597 CGTGCAGTGTCCGGGAAAAACAGTGAAAAAATATCATGAGGTGCTGAAAATTTGCTCCCGAGGC	656		
Qy	AYATHAARMGNGMNGMNGNCA	1033		
Db	657 GGAGCATTCCTCCGAAAGAAAGGCAA	680		

Search completed: November 15, 2004, 20:15:25

Tue Nov 16 16:09:48 2004

us-09-876-813-6.rst

Page 14

Job time : 5895.35 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 15:30:46 ; Search time 143.177 Seconds
(without alignments)
5510.484 Million cell updates/sec

Title: US-09-876-813-6

Perfect score: 1110

Sequence: 1 atgcagmgnytnathtygt.....gyanwmnmgncnccmgn 1110

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798	71.9	1110	4	US-09-564-595D-6
2	798	71.9	1882	4	US-09-457-066-36
3	798	71.9	1882	4	US-09-540-224-1
4	798	71.9	1882	4	US-09-564-595D-1
5	798	71.9	1882	4	US-09-706-968-36
6	798	71.9	1882	4	US-09-808-972-1
7	798	71.9	2253	4	US-09-438-046-7
8	757.4	66.2	1162	4	US-10-140-002-185
9	714.8	64.4	1472	4	US-09-540-224-3
10	714.8	64.4	1472	4	US-09-564-595D-52
11	714.8	64.4	1472	4	US-09-808-972-3
12	697.6	62.8	1934	4	US-09-438-046-5
13	406.4	36.6	690	4	US-09-438-046-3
14	186.4	16.8	1035	4	US-09-457-066-6
15	186.4	16.8	1035	4	US-09-706-968-6
16	177.6	16.0	1035	4	US-09-468-647-3
17	177.6	16.0	1095	4	US-09-457-066-50
18	177.6	16.0	1095	4	US-09-706-968-50
19	177.6	16.0	1760	4	US-09-457-066-1
20	177.6	16.0	1760	4	US-09-564-595D-32
21	177.6	16.0	1760	4	US-09-706-968-1
22	177.6	16.0	1760	4	US-09-823-033-1
23	177.6	16.0	2825	3	US-09-040-220D-1
24	177.6	16.0	2825	4	US-09-265-686-1
25	177.6	16.0	2825	4	US-09-723-749-1
26	177.6	16.0	2849	4	US-10-140-002-285
27	175	15.8	3571	4	US-09-457-066-42

28	175	15.8	3571	4	US-09-564-595D-34	Sequence 34, Appl
29	175	15.8	3571	4	US-09-706-968-42	Sequence 42, Appl
30	175	15.8	3571	4	US-09-823-033-3	Sequence 3, Appl
31	144.8	13.0	360	4	US-09-438-046-1	Sequence 1, Appl
32	103.2	9.3	504	4	US-09-468-647-28	Sequence 28, Appl
33	87	7.8	1141	4	US-09-806-708B-22	Sequence 22, Appl
34	78	7.0	1141	4	US-09-806-708B-22	Sequence 22, Appl
35	77	6.9	452	4	US-09-621-976-1352	Sequence 1352, Ap
36	68	6.1	600	4	US-09-564-595D-36	Sequence 36, Appl
37	64	5.8	1055	4	US-09-806-708B-23	Sequence 23, Appl
38	61.2	5.5	832	4	US-09-621-976-2813	Sequence 2813, Ap
39	59.6	5.4	2169	4	US-09-434-408-3	Sequence 3, Appl
40	58.6	5.3	7218	1	US-08-232-463-14	Sequence 14, Appl
41	57.2	5.2	474	4	US-09-621-976-18033	Sequence 18033, A
42	56.2	5.1	505	4	US-09-621-976-15639	Sequence 15639, A
43	55.6	5.0	1110	4	US-09-564-595D-6	Sequence 6, Appl
44	54.2	4.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
45	53.8	4.8	399	4	US-09-621-976-8976	Sequence 8976, Ap

ALIGNMENTS

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RESULT 1
US-09-564-595D-6
; Sequence 6, Application US/09564595D
; Patent No. 6435668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-564-595D-6

Query Match          71.9% Score 798; DB 4; Length 1110;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGCAGMGYTNATHHTYGTNTAATNTATHTGYGCNAAYTTGYVSNMGNGAY 60
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QY 61 ACNWSNGCNAACCCNCAKWSNCSNATHAAGCYTTMGAAAYGCNAAYTTNGMNG 120
    |||||
DB 61 ACNWSNGCNAACCCNCAKWSNCSNATHAAGCYTTMGAAAYGCNAAYTTNGMNG 120
    |||||

QY 121 GAYGARMSNAACAYTTNACGAYTTNTAYMGNGAYGARACNATHCARGTNAARGN 180
    |||||
DB 121 GAYGARMSNAACAYTTNACGAYTTNTAYMGNGAYGARACNATHCARGTNAARGN 180
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QY 181 AAYGNTAYGTNCARMSNCCMNGNTTYCCNAAYWSNTAYCCMNGNAAYTTNTYTNACN 240
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DB 301 YTNNGARGARCGNRAAAYGAYATHGYMGNTAYGAYATYTGNGARGTNGARGAYATHMSN 360
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DB 361 GARACMSNACNATHATHMNGMNGMTGTGTGNGNCAVAAARGRTNCCNMGNAATH 420
QY 421 AARMSNMGNAACNAYCARATHAARATACNTTYAARMSNAGAYATYATYTGNGNCAAR 480
DB 421 AARMSNMGNAACNAYCARATHAARATACNTTYAARMSNAGAYATYATYTGNGNCAAR 480
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DB 481 CNGGNTTYAARATHATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 540
QY 541 ACNAAATYGGARWSNGTNAACMSMSNATHTMSNGNGTMSNTAYAAVMSNCCMSNGTN 600
DB 541 ACNAAATYGGARWSNGTNAACMSMSNATHTMSNGNGTMSNTAYAAVMSNCCMSNGTN 600
QY 601 ACNGAYCNAACNTTNAATHGNGAYGNTNGAYAAABARATGCGNARTTYGAYACNGTN 660
DB 601 ACNGAYCNAACNTTNAATHGNGAYGNTNGAYAAABARATGCGNARTTYGAYACNGTN 660
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DB 661 GARGAYTYTNAARATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 720
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DB 781 GAYMGNTYTAAGAYACNAARMGNTAYMSNTGYACNCCMNGNAAATYATYMSNGTNAAY 840
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DB 1021 MNGMNGMNGNCAARACNATGCGNTNGTNGAYATHTCARNTNGAYCAVAYGARGMNTGY 1080
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DB 1081 GAYTYATHTGYMSWMSMNGNCCNCCNG 1109

RESULT 2

US-09-457-066-36

Sequence 36, Application US/09457066

Patent No. 6432673

GENERAL INFORMATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Piddington, Christopher S.

APPLICANT: Shepherd, Paul O.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 1882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (226)... (1338)
US-09-457-066-36

Query Match 71.9%; Score 798; DB 4; Length 1882;

Best Local Similarity 56.4%; Pred. No. 4.7e-231; Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCATYMGNTYNAATHHTYTGNTAYACNTYNAATHHTGYCNAATYTYGYMSNTGYMGNGAY 60
DB 226 ATGCACCGCTCATCTTGTCTACACTTAATCTGCCAACTTTGACGCTGTCCGGAC 285
QY 61 ACNMSNGNACNCCNCAARMSNCGMNSNATHAARCGNTNMNAAVGCNAAATYTMGMNGN 120
DB 286 ACTTCTGCAACCCCGAGCGCATCAATCAACCTTTGGCAACGCCAAGCTGACGCA 345
QY 121 GAYARMSNAAVCAATYTNACNGAYTNTAYMNGMNGAYGABACNATHCARGTNAARGN 180
DB 346 GATGAGAGCATCACTCACAGACTGTACGMAAGATGAGACATCCAGTGAAGAAGA 405
QY 181 AAYGNTAYGNTCAARMSNCCMNGTTCNAAVMSNTAYCCNMGNAATYNTYNTYACN 240
DB 406 AACGCTACGCGCAAGTCTTGAATTCGCCAAGCTACCCAGGAACCTGCTCTGACA 465
QY 241 TGGMNGNTNCAWNSNCARGAARAACMNGNATHCARTYNGNTTYGAYAAVCAATYNGN 300
DB 466 TGGGCGCTTCACTCTCAGGAATPACAGATACGTAAGTTTGACATCGATTGGA 525
QY 301 YTNNGARGARCGNRAAAYGAYATHGYMGNTAYGAYATYTGNGARGTNGARGAYATHMSN 360
DB 526 YTNNGARGARCGNRAAAYGAYATHGYMGNTAYGAYATYTGNGARGTNGARGAYATHMSN 360
QY 361 GARACMSNACNATHATHMNGMNGMTGTGTGNGNCAVAAARGRTNCCNMGNAATH 420
DB 586 GAAACCGTACCTTATTTAAGAGACGATGTGGAACAAAGAAAGTTCTCCAAAGATA 645
QY 421 AARMSNMGNAACNAYCARATHAARATACNTTYAARMSNAGAYATYATYTGNGNCAAR 480
DB 646 AATCAAGAACGAACAAATTAATCACTTCAAGTCCGATGACTTATGCTGCTTAA 705
QY 481 CNGGNTTYAARATHATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 540
DB 706 CCGGATTCAGATTAATTAATTTCTTGTGGAAGATTTCCAAACCCAGAGCTTCAGAG 765
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DB 886 GAAATCTGCTCAAGTACTTCAATCCAGTATGCAAGAAAGATCTTGAAGATATGAT 945
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DB 946 CTGGAACACCCCTCGGATGAGAGGATCATCATGACCGGAATGCAAAATTTGACCTG 1005
QY 781 GAYMGNTYTAAGAYACNAARMGNTAYMSNTGYACNCCMNGNAAATYATYMSNGTNAAY 840

Db 1006 GATAGGCTCATGTATGATGCCAAGGCTTACAGTTSCATCCCAAGAAATTACTCGTCAAT 1065
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Db 1066 ATAAGAGAAGAGCTGAAGTGGCCCAATGTGTCTTCCATCGTTGGCTCTCTGTGAG 1125
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Db 1186 GGGAAACCGTGAABAAATATCATGAGGTATTAAGCTTGAAGCCGTGGCCATCAAGAG 1245
Qy 1021 MGNNGMNGCNAARACNAATGCGNTYNTNGAYATHCARNTNGAYCAVARGMNTGY 1080
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Db 1306 GATTGTATCTGACGCTCAAGACCACTCTCG 1334

RESULT 3

US-09-540-224-1
; Sequence 1, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-540-224-1

Query Match 71.9%; Score 798; DB 4; Length 1882;

Best Local Similarity 56.4%; Pred. No. 4,7e-231; Mismatches 183; Indels 0; Gaps 0;

Db 1 ATGCAVMGNTNATHTTGTNTAYACNTYNTATHTSYGCAAAVTTTGYMSNTGYMNGAY 60
Qy 226 ATGCAACGGCTCATCTTTGTCTACACTTAATCTGCGAAACTTTTGAAGCTGTGGAG 285
Db 61 ACNMSNGCNAACCCNARMSNGCNSNATTHAARGNTYNTMNGAAYGCNAAYTMMNGN 120
Qy 286 ACTTCTGCAACCCCGACAGCGCATTCATAAAGCTTTGGCGAAGCCCACTCAAGCGCA 345
Db 121 GAYGARMSNAAYCAVYNTNACGAYTNTYNTMNGMNGAYGARACNAATCARTNABRN 180
Qy 346 GATGAGCAATCACTTGAACGCTTGAACGAGATGAGACCATCCAGGTGAAGGA 405
Db 181 AAYGNTAYGTNCAARMSNCNMNGNTTCCNAAYMSNTAYCCMNGAAYVYNTYNTNACN 240
Qy 406 AACGCTACGTGCAAGAGCTTAGATTCCCGAACACTACCCAGAGAACCTGTCTGACA 465
Db 241 TGGMNTNCAVMSNCARAGARAAYACNMGNATHCARNTYNTTGYAAYACARTTYGCN 300
Qy 466 TGGCGGCTTCACTCTCAAGAGAAATACAGGATACAGTAGTGTGACAAATCAGTTTGA 525

Qy 301 YTNARGARGCNGARAAYATHTGYMNTAYAGATYTTGNGARGINGARGAYATHWSN 360
Db 526 TTAGAGGAAGCAAAAATGATATCTGTAGTATGATTTTGTGGAAGTTGAGATATATCC 585
Qy 361 GARACMSNACNATHATHTMNGMNGMNTGTGTGYGNCAYARARGNTCCNMGNATH 420
Db 586 GAAACCACTACATATATAGAGAGCATGTGTGTGACCAAGAGATGTTCTTCAAGATYA 645
Qy 421 AARMSNMNACNAAYCARATHAARATHACNTTYAARMSNGAYGATVATYTTGNCNAR 480
Db 646 AAATCAAGACGAACCAATTAATTAATCAATTCAGATCGATGACTTGTGTGCTTAA 705
Qy 481 CCNGNTTYAARATHATAYATYMSNTYNTNGARGAYTYTCARCCNGCNGCNGMNGAR 540
Db 706 COTGATTCAGATTTATATTATTCTTGTGTGAAGATTTCCAACCGGACGAGCTTCAAG 765
Qy 541 ACNAAVYTGARGMSNGTACNMSWSNATHTMSNGNGTMSNTAYAAVMSNCMSNGTN 600
Db 766 ACCAAGTGGGAATCTGTCAAGAGCTTATTCAGGGGTATCTTAACTTCCATCAAGTA 825
Qy 601 ACNAGVCCNACNTYNTATHTGNCAYGANTYNGAYARABATHGNGARTTYGAYCNGTN 660
Db 826 ACGATCCCACTGTGATGCGAGTGTCTGACCAAAAATTTGCAAAATTTGATACAGTG 885
Qy 661 GARGAYTNTYNTAARTATYTYAAYCCNGARMSNTGCGARGARGAYTYNGARAAYATGY 720
Db 886 GAAGATCTGCTCAAGTACTTCAATCCAGATCATGCAAGAGANTCTTGAGATATGAT 945
Qy 721 YTNAGVACNCCMNTAYMNGMNGMNSNTAYCAVYMGNAARMSNARGTNGAYTN 780
Db 946 CTGACACCCCTCGGTATGAGGAGCGAGCTCATACCATGACCGAAGTCAAAAGTTACCTG 1005
Qy 781 GAYMNTNAYVAGAYGACNAARBMGNTAYMSNTGYACNCCMNGAATAYATVMSNTAY 840
Db 1006 GATAGGCTCAATGATGCGCAAGGCTTACAGTTGACTCCAGGAATTTACTCGTCAAT 1065
Qy 841 ATHMNGARGARYTNAARYTNGCNAAYTNGTNTTYYTCCMNGTYTNTYNTNGCAR 900
Db 1066 ATAAGAGAAGAGCTGAAGTGGCCCAATGTGTCTTTCACAGTTGGCTCTCTGTGAG 1125
Qy 901 MGNTRYGNGNNAAYTGYGNTGYGNAACNGTNAAYTGAMGMSNTGYACNTGYAAYSN 960
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Db 1186 GGGAAACCGTGAABAAATATCATGAGGTATTAAGCTTGAAGCCGTGGCCATCAAGAG 1245
Qy 1021 MGNNGMNGCNAARACNAATGCGNTYNTNGAYATHCARNTNGAYCAVARGMNTGY 1080
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Db 1306 GATTGTATCTGACGCTCAAGACCACTCTCG 1334

RESULT 4

US-09-564-595D-1
; Sequence 1, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: US 60/180,169
 PRIOR FILING DATE: 2000-02-04
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1882
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (226)...(1338)
 US-09-564-595D-1

Query Match 71.9%; Score 798; DB 4; Length 1882;
 Best Local Similarity 56.4%; Pred. No. 4,7e-231;
 Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

1 ATGCAYMGNVYNAHTTGTNTAAYACNYTNAHTGTGCAAAATTTGTGWSNTGNGAY 60
 226 ATGCACCGGCTCATCTTGTCTACCTTAATCTGGCAAACTTTTGCAGCTGTGGGAC 285
 61 ACNWSGCAACNCCNARNSNCNMSNATHARGCNTTMMGAAATGCAATTTNNMGN 120
 286 ACTTTCGCAACCCCGAGAGCCATCCATCAAGCTTTGGCAAGCCCACTCAGGCGA 345
 121 GAYGARSNAAYCAAYTNAACGAYTNTAYMGNMGAYGABACNATHCARGTNAARGN 180
 346 GATGAGAGCAATCACCCTCAACAGCTTGTACCGAAGAGTAGACATCCAGGTGAAGA 405
 181 AAYGNTAYGTCNARNSNCNMGNTTCCNAAATWSNTAYCCMGNAAATTTNTYNA 240
 406 AACGGCTACGTCAAGTCTTAGATTTCCGAAACAGTACCCGAGAACCTGCTCTGACA 465
 241 TGMGNNTYCAWSNCARGAARAAYACNMGNTATHCARYNTGNTTGAAYCAATTTG 300
 466 TGGCGGCTTCACTCTCAGAGAAATACAGGATACAGCTAGTGTGACAAATCAATTTGA 525
 301 YTMGARBARCNGAPAYGAYATHTGNGNTAYGAYTTTGTGARGTNGARAYATHSN 360
 526 TTAGAGGAAGCAGAAATGATATCTGATGATGATTTTGTGGAAGTTGAATATATCC 585
 361 GABACNMSNACNATHATMGNGMNGNTGTGTCGNCAYARBARGTNCNMGNTATH 420
 586 GAATCAGATCATTAATTAAGAGAGATGTGTGACCAAGAGATTCCTCCAAAGGATA 645
 421 AARWSNMGACNAAACARATHAARATHACNTTAYARWSNGAYATYATTTGTGCAUAR 480
 646 AAATCAAGAACCAATTAATTAATCAATTCAGTCCAGTACTTGTGTGCTTAA 705
 481 CCNGNTTAAATHTATTAATWSNTTNTNGARAYTTTCARCCNGCNGCNGCNGAR 540
 706 CCGATTCAGATTAATTAATTTCTTGTGCAAGATTTCCAAACCGGACGAGCTTCAAG 765
 541 ACNAAATYGGARWSNGTNAACNWSMNSNATHWSNGNNGMNTYAAATWSMCCNWSMNTN 600
 766 ACCAACTGGGATCTGTCAACAAGCTTATTTCAAGGGATCTCTTAATCTCCATCAAGTA 825
 DB 886 GAAGATCTGTCAAGTACTTCAATCCAGAGTCAAGGAGAAAGATCTTGGAAATATAT 945
 QY 601 ACNGAYCCNACNYTNAHTGNCAGVGYNTNGAYARAARATHGNCARATTTGAYACNGTN 660
 DB 826 ACGGATCCCACTGATGTCGAGATGCTCTGGAACAAAATTTGCAAGATTTGATACAGTG 885
 QY 661 GARGVYNTNARATVYTAAYCCNAGARWSNTGGCARBARGYNTNGARAAATGTAY 720
 DB 946 CTGAGACACCTCGGTATCGAGGAGGATCAATACATACCGGAGAGTCAAAAGTTGACTG 1005
 QY 721 YTMGARBARCNGAPAYGAYATHTGNGNTAYGAYTTTGTGARGTNGARAYATHSN 780
 DB 946 CTGAGACACCTCGGTATCGAGGAGGATCAATACATACCGGAGAGTCAAAAGTTGACTG 1005
 QY 781 GAYGNTAYGTCNARNSNCNMGNTTCCNAAATWSNTAYCCMGNAAATTTNTYNA 840
 DB 1006 GATGAGTCAATGATGATGTCGAGATGCTTACAGTGTGCACTCCAGGATTAATCTCGTCAAT 1065

QY 841 ATHMNGARBARVYNTAARYTNGCAAAVGTGNTTNTTTCNMGNTGYTNTYNTNGAR 900
 DB 1066 ATAAGAGAAAGAGCTGAAGTGTGGCAATGTGTCTTCTTCCAGGTGTGCTCTGTGAG 1125
 QY 901 MGNTRYGNGNNAAYTGTGNTGTGCAACNCTNAAYTGAMNSNTGYACNTGYAATWSN 960
 DB 1126 CGCTGTGAGAAATTTGTGCTGTGGAACGTGTCACTGAGAGTCTGTGCAATGCAATTTCA 1185
 QY 961 GGNARACNCTNARAAATAYCAVARGTNTNCAATTTGARGCCNGCNGCAVATAARMGN 1020
 DB 1186 GCGAATAACCGTGAATAAAGATACATGAGGTATTAAGTTGAGCTTGCCCATCAAGAGG 1245
 QY 1021 MGNMGNGNCAARACNATGTGCTTGTGNTGNTGATHTCARVYNTGAYCAVARGMNTGY 1080
 DB 1246 AGGGTGTGAGCTAAGACATGTGCTTAGTGTGACATTCACATGATGATCAATGAACGATGC 1305
 QY 1081 GAYTATHTGTGWSMNSMNCNCCNMG 1109
 DB 1306 GATGTATCTGACGTCAAGACCACTG 1334

RESULT 5
 US-09-706-968-36
 Sequence 36, Application US/09706968
 Patent No. 6528050
 GENERAL INFORMATION:
 APPLICANT: Gao, Zeren
 APPLICANT: Hart, Charles E.
 APPLICANT: Piddington, Christopher S.
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Shoemaker, Kimberly E.
 APPLICANT: Gilbertson, Debra G.
 APPLICANT: West, James W.
 TITLE OR INVENTION: GROWTH FACTOR HOMOLOG ZVEG3
 FILE REFERENCE: 98-60C1
 CURRENT APPLICATION NUMBER: US/09/706,968
 CURRENT FILING DATE: 2000-11-06
 PRIOR APPLICATION NUMBER: US/09/541,752
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 36
 LENGTH: 1882
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (226)...(1338)
 US-09-706-968-36

Query Match 71.9%; Score 798; DB 4; Length 1882;
 Best Local Similarity 56.4%; Pred. No. 4,7e-231;
 Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

1 ATGCAYMGNVYNAHTTGTNTAAYACNYTNAHTGTGCAAAATTTGTGWSNTGNGAY 60
 226 ATGCACCGGCTCATCTTGTCTACCTTAATCTGGCAAACTTTTGCAGCTGTGGGAC 285
 61 ACNWSGCAACNCCNARNSNCNMSNATHARGCNTTMMGAAATGCAATTTNNMGN 120
 286 ACTTTCGCAACCCCGAGAGCCATCCATCAAGCTTTGGCAAGCCCACTCAGGCGA 345
 121 GAYGARSNAAYCAAYTNAACGAYTNTAYMGNMGAYGABACNATHCARGTNAARGN 180
 DB 346 GATGAGAGCAATCACCCTCAACAGCTTGTACCGAAGAGTAGACATCCAGGTGAAGA 405
 QY 181 AAYGNTAYGTCNARNSNCNMGNTTCCNAAATWSNTAYCCMGNAAATTTNTYNA 240
 DB 406 AACGGCTACGTCAAGTCTTAGATTTCCGAAACAGTACCCGAGAACTGCTCTGACA 465
 QY 241 TGMGNNTYCAWSNCARGAARAAYACNMGNTATHCARYNTGNTTGAAYCAATTTG 300
 DB 466 TGGCGGCTTCACTCTCAGAGAAATACAGGATACAGCTAGTGTGACAAATCAATGTTGA 525

PRIOR APPLICATION NUMBER: US 09/564,595
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: US 60/180,169
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/164,463
 PRIOR FILING DATE: 1999-11-10
 PRIOR APPLICATION NUMBER: US 60/132,250
 PRIOR FILING DATE: 1999-05-03
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 1882
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (226) ... (1338)
 US-09-808-972-1

Query Match 71.9%; Score 798; DB 4; Length 1882;
 Best Local Similarity 56.4%; Pied. No. 4,7e-231;
 Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0

QY	1	ATGCAYMGVNTAATHTTGTGTATYACNNTYNAATHGTGCGNAAYTTTGYGMSNTGIMGNGAY	60
DB	226	ATGCACCGGCTATCTTTGTCTACACTCTAATCTGCGCAAACTTTGCGAGCTGTGGAC	285
QY	61	ACNWSNGCNAACNCNCARMSNGCMNSNATHAARGCNYTMGNAAYGCNAAYTTNMGMN	120
DB	286	ACTCTGCAACCCCGACAGCGCATCATCAAGCTTTGGCAACGCAACTCAGCGCA	345
QY	121	GAYGARMSNAAYCAYTTNACNGAYTTNTYTMGMNGAYGARCAATHCARGTNAARGN	180
DB	346	GATGAGGCAATCACCTCAACACTGTGACCGAAGATGAGACCATCCAGGTGAAGA	405
QY	161	AAYGNTATGTCARMSNCNMNGTTCNAAVMSYTAACNMGNAAVYNTNTYNAACN	240
DB	406	AACGGCTACGTGACAGGTCTTGATTTCCGAACAGCTACCCAGAACTGCTCTGACA	465
QY	241	TGCMGNTYTCAYMSNCARGARAAYACNMGNATHCARVYNTGNTTYGAAVCAATTYGN	300
DB	466	TGGCGGCTTCACTCTCAGAGAAATCACGGATACAGCTAGTGTTCACATCAGTTTGA	525
QY	301	YTMGARARGCNGARAAVAYVTHGTGMENTYAGATYTTGTNGARGTNGARAYATHWSN	360
DB	526	TTAGAGGAAGCAGAAATGATATCTGTAGATYATGATTTGTGGAAGTTGAAGATATATCC	585
QY	361	GARACMSNACNAATHATMGNGCMNGTGTGACAAVBARARGTNCNCCNMGNATH	420
DB	586	GAACACAGTACCATTAATTTAGAGACGATGTTGGACACAAAGAAAGTCTCTCAAGGATA	645
QY	421	AARMSNGACNAACARATHAARATHAACNTTYAARMSNGAYAYATYTTGTNGCAAR	480
DB	646	AAATCAAGAACCAACCAATTAATAATCAATTCAGATCCGATACATCTTTGTGGCTAAA	705
QY	481	CCNGGNTTYAARATHTATYATVMSNTYNTYNGARGATYTCARCNGCNGCNGMSNGAR	540
DB	706	CTTGATTCACAAATTTATATTCTTGTGCGAAGATTTCCACCACCCGACAGCTTCAGAG	765
QY	541	ACNAAYTGGAARMSGTNACMSMSNATHMSNGGTMMSNTAYAAVMSNCCNMSGNTN	600
DB	766	ACCAACTGGGAATCTGTCAAGAGCTCTATTTCAGGGGATCTCTATACCTTCATCACTGA	825
QY	601	ACNGAYVCCNAACNYTATHTGCGNAYGCGNTYNTGAYVAAARAAATHTGCGNARATTYGACNTN	660
DB	826	ACGATTCACACTCTGATTTGCGATGTCTGCGACAAATAATTCAGAAATTTGATACAGTG	885
QY	661	GARGAYTNTYNAARTATYTTAYVCCNGARMSNTGCGARGARGAYTTNGARAAVATGTAY	720
DB	886	GAAGATCTGCTCAAGTACTTCAATCCAGAGTCAAGTCAAGAAAGATCTTTGGAATATGTAT	945
QY	721	YTMGAYACNCNMGTATVMGNGCMNSNTAYCANGATMGNAARMSNARGNTNGAYTNT	780

Db 946 CTGACACCCCTCGTATGAGGCAAGTCAATACCATGACCGGAAGTCAAAAGTTGACTTG 1005
Qy 781 GATMGTNTAAAYGAYGACNAARMGNTAATWSTGTACNCCNMGNAAYTAAYMSNGTAA 840
Db 1006 GATAGGCTCAATATGATGACCAAGCCGTTCACAGTTGACCTCCAGAAATTAATCTGCTCAAT 1065
Qy 841 ATMGNGARGARYTNAARYTNGCNAAYGTGNTTCTTCCNMGNTGYTNTNGNCAR 900
Db 1066 ATAGAGAGAGAGTGAAGTTGGCCATGTGTCTTCTTCCAGTTGCTGCTCCCTCGTGAG 1125
Qy 901 MENTGYGNGGNAAYTGYGANTGYGNAACNTNAAYTGGMWSTGYACNTGYAAYMSN 960
Db 1126 CGCTGTGGAGAAATGTGCTGTGTGAACTGTCACTGGAGAGTCTGCAATGCAATTC 1185
Qy 961 GGNAPACNGTNAARATTAAYGARGNTNCAATTTTGACCGNGCAATTAARMN 1020
Db 1186 GGGAAACCGTGAAGAAATGATCTAGGATTAATCACTTTGAGCTGGCCACATCAAGAG 1245
Qy 1021 MNGNGMNGCNAARACNAATGGCNYTNGTNGAATTHCARVTNGAYCAAYGARGMNTGY 1080
Db 1246 AGGGGTAGAGCTTAAGACCATGCTGCTAGTTGACATTCAGTTCATCAATGCAATGC 1305
Qy 1081 GATGYAATHTGYMSNMNGNCNCNMG 1109
Db 1306 GATGTATCTGACGCTCAAGACCACTCG 1334

RESULT 7
US-09-438-046-7
Sequence 7, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: ERIKSSON, Karin
APPLICANT: AASE, Karin
APPLICANT: PONTN, Annika
APPLICANT: LEE, Xuri
APPLICANT: LUTTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
EARLIER FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 2253
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (176)..(1288)
US-09-438-046-7

Query Match 71.9%; Score 798; DB 4; Length 2253;
Best Local Similarity 56.4%; Pred. No. 5,7e-211;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
Qy 1 ATGCAVNGTNTAAHTTGTGNTTAACNTTAATHTGACNAAYTTTGYGNTGNGAY 60
Db 176 ATGCAACGGGCTCATCTTGTCTACACTTAATCTGCGCAAACTTTGACGCTGCGGAC 235

Qy 61 ACNMSGNCAACNCCNARMSGNCAATHAAGCNTTNGMNAAYGCAAYTNTMNGN 120
Db 236 ACTTGTGACCCCGGAGAGGACATCCATCAAGCTTTGGCAACGCCAAGCTCAGGCA 295
Qy 121 GAYGARSNAAYCAATYTAACGATYTTNTAYGNNNGAYGARGACNATHCARGTNAARGN 180
Db 296 GATGAGCAATCACTCAAGACTTGTACGAAGATGAGACCATCCAGGTGAAAGGA 355
Qy 181 AAYGNTYGTNCARMSGNCAATYCCNAAYSNTAYCCNMNAAAYTNTYNTA 240
Db 356 AACGCTACGTCGAGAGCTTCAATTTCCCAACGCTACCCAGAACGCTGCTGCA 415
Qy 241 TGMGNTYTCAYMSNCARGAARAAVACNMGNATHCARVTNGTNTGYAAYCARTTYGN 300
Db 416 TGGCGGCTTCACTCTCAGAGAAATACAGGATACAGTAAGTGTGCAATCAATTTGGA 475
Qy 301 YTNARGARGCGNARAAYGATHTGYMNTAATYTTGTNGARGTNGARGAYATHMSN 360
Db 476 TTAGAGAGAGAAATGATATCTGATGATGATTTGTGAAAGTTGAAGATATATCC 535
Qy 361 GARAAMSNACNATHATMGNGMNTGTGAGCAAYARGARNTCCNMGNATH 420
Db 536 GAACACAGTACATTAATTAGAGAGATGTGTGACACAAAGAACTTCTCCAGATA 595
Qy 421 AARMSNMGACNAAYCARATHAARATHACNTTAAARMSNGAYATYTTGTNGCAAR 480
Db 596 AAATCAAGAACGAACCAATTAATAATCAATCAAGTCCATGATCTTGTGCTAAA 655
Qy 481 CCNGNTTAAARATHTAYTAYMSNTYNTGARGAYTTTCARCCNGCNGNMSGAR 540
Db 656 CCGGATTTCAAGATTTATTTCTTCTGCTGAGAAATTTCCAAACCCGAGAGCTTGAG 715
Qy 541 ACNAAYTGGARGARMSGTNAACNMSNSNATHMSGNGTMSNTAYAAAYMSNCCNMSGTN 600
Db 716 ACCAACTGGGAATCTGCAACAGCTCATTTCAAGGGATCTATATACTTCATCAGTA 775
Qy 601 ACNAYCCNACNTNTATGNGAYGNTYNTGAARAAARATHCCNARPTTGYAACNTN 660
Db 776 ACGATCCACTGTTGATGAGATGCTGAGCAAAAATTTGCAAAATTTGATACAGTG 835
Qy 661 GARGAYTNTAARTAYTTTAAATCCNGARMSNTGCGARGARAYTNGARAATGTAY 720
Db 836 GAAGATCTGCTCAAGTACTCAATCCAGGTACATGCAAGAAAGATCTTGAAATATGTA 895
Qy 721 YTNAGAACNCCNMGNTAYMNGMNGMNTAYCAATGATMNAARMSNARGTNGAYTN 780
Db 896 CTGACACCCCTCGTATGAGGACAGGTATCCATGACCGGAAAGTCAAAAGTTGACCTG 955
Qy 781 GAYMGTNTAAAYGAYGACNAARMGNTAATWSTGTACNCCNMGNAAYTAAYMSNGTAA 840
Db 956 GATAGGCTCAATATGATGACCAAGCTTACAGTTGACCTCCAGAAATTAATCTGCTCAAT 1015
Qy 841 ATMGNGARGARYTNAARYTNGCNAAYGTGNTTCTTCCNMGNTGYTNTNGNCAR 900
Db 1016 ATAGAGAGAGAGTGAAGTTGGCCATATGTGCTTCTTCCAGTTGCTCTCCGTGAG 1075
Qy 901 MENTGYGNGGNAAYTGYGANTGYGNAACNTNAAYTGGMWSTGYACNTGYAAYMSN 960
Db 1076 CGCTGTGGAGAAATTTGTGCTGTGAACTGTCACTGGAGGTCTGCAATGCAATTC 1135
Qy 961 GGNAPACNGTNAARATTAAYGARGNTNCAATTTTGACCGNGCAATTAARMN 1020
Db 1136 GGGAAACCGTGAAGAAATGATCATGAGTTTACAGTTTGAAGCTGCGCAATCAAGAG 1195
Qy 1021 MNGNGMNGCNAARACNAATGGCNYTNGTNGAATTHCARVTNGAYCAAYGARGMNTGY 1080
Db 1196 AGGGGTAGAGCTTAAGACCATGCTGCTAGTTGACATTCAGTTGATCAACATGAAGATGC 1255
Qy 1081 GATGYAATHTGYMSNMNGNCNCNMG 1109
Db 1256 GATGTATCTGACGCTCAAGACCACTCG 1284

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RESULT 8
US-10-140-002-185
; Sequence 185, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; PRIOR FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 185
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-185

Query Match      68.2% Score 757.4; DB 4; Length 1162;
Best Local Similarity 55.6%; Pred. No. 5.9e-219;
Matches 617; Conservative 294; Mismatches 180; Indels 18; Gaps 1;

QY 1 ATGCAGMGNATNTATTTTGTATACNTATNTATTTGTCGCAATTTTGTGMSNTGTMNGAY 60
DB 32 ATGCACCGGCTCATCTTGTCTACACTCACTCACTCGGCAACTTTTGCAGCTGTGGGAGC 91
QY 61 ACNMSNGCNAACCCCAACMSNGCNSNATHARCGNTTNGMAAYGCNAAYTTMNGMNGN 120
DB 92 ACTCTGCAGACCCCGCAGAGCGCATCCATCAAGCTTTGCGCAGCCCACTCGAGGGA 151
QY 121 GAYGARMSNAAYCAVYTNACNGAYTTNTAYMGMNGAYGARACNATHCARGTNARGN 180
DB 152 GAT-----GACTTGTCGAGAGATGAGACCATCCAGGTGAGAGGA 193
QY 181 AAYGNTATGTCARMSNCNMNGNTTCCNAAYMSNTAYCCMNGNAAYTTNTYTNACN 240
DB 194 AACGCTACGTGCAAGTCTGATGATTCGCCGAAACACTACCCAGAGACCTGCTCGACA 253
QY 241 TGGMNTTNCAYWSCNARAGARAAYCCNMGNATHCARNTGNTTGYAAYCARTTTGGN 300
DB 254 TGGCGGCTTCACTCTCAGAGAAATACAGGATACAGCTAGTGTGACACATCAGTTTGA 313
QY 301 YTNAGRGARCGNARAAAYATHTGYMGNATYGYATTTGNTGARGTNGARGAAYTHMSN 360
DB 314 TTAGAGAGAGCAAGAAATGATATCTGTAGGTATGATTTTGTGAAGTTGAAATATATCC 373
QY 361 GARACMSNACNATHATHTGNGMNGNTGTYGNCAYAAARGATNCNCNMGNATH 420
DB 374 GAATACAGTACATATATAGAGAGAGATGTGTGACACAAAGAACTCTCCAGAGATA 433
QY 421 AARMSNMGACNAAYCARATTAARATTHACNTTAAARMSNAGAYATYTTTGTNGNAR 480
DB 434 AATATCAAGAACCAACCAATTTAAATTCACATTCAGTCCGAGTACTTGTGTGATAA 493
QY 481 CCGNNTTAAATTAATTAAYASNTNTYNGARGAATTCACGCGCNGCNCNMNGAR 540
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DB 494 CTGGATTCAGAGATTATTTATTTCTTGTGAGAGATTTCCAACCCGAGAGCTTCAGAG 553
QY 541 ACNAAYTGGARMSNGTNAACMSMSNATHMSNGCNGMNTAATAAATMSNCMSNGN 600
DB 554 ACCAATCGGAATGTCACAAAGCTTATTCAGGGGTATCTTAACTCTTCACAGTA 613
QY 601 ACNGAYCCNANTYNAATHGNGAYGVCNTYTNAAARARATHGNGARTTYGAYACNGTN 660
DB 614 ACGATCCCACTCTGATTTGCGGATCTCTGACACAAAAAATTTGCAGATTTGATCAGTG 673
QY 661 GARGAAYTNTAAATATYATTAAYCCNGARMSNTGCGARGARAYTNGARAAAYTAY 720
DB 674 GAAGATCTGTCAAGTACTTCATTCACAGATCATGCAAGAAAGATCTTGAGATATGTAT 733
QY 721 YTNAGAYACNCCMGTATMNGMNGMNSNTAYCAYAYMGNAAARMSNAAAGTNCAYTN 780
DB 734 CTGACACCCCTCGGTATCGAGGCGATCATACCAATCCGGAAGTCAAAAGTTGACCTG 793
QY 781 GAYMGNNTAAAYGAYGACNAARBMGNTAYMSNTGYACNCCMNGAAYTAAYMSNTAA 840
DB 794 GATAGGCTCAATGATGATGCGCAAGCTTACATTCACATCCAGAAATTAATCTCGGTCAAT 853
QY 841 ATHMNGARGARAYTNAATYTNACNAAYGTNGTNTTTCYCCMNGTGYTNTYNGTCAR 900
DB 854 ATAAGAGAAAGAGCTGAAGTGGCCAAATGCTTCTTCCAGCTTGCTCCTCGTGAG 913
QY 901 MGNATYGGNGNAAYTGTGNTGYGNAACNGTNAAYTGGMGMSNTGYACNTGYAAYMSN 960
DB 914 CGCTGTGAGGAAATTTGTGGCTGTGGAATCTGCACTGAGAGTCTTGACATGCAATTTCA 973
QY 961 GGNARACNGTNAARATTAAYCAVARGTNTYTCARTYTGARCCNGCNAAYTAARBMGN 1020
DB 974 GGGAAACCGTGAAATAATATCATAGATATTAAGCTTTGAGCTGCGCACATCAAGAG 1033
QY 1021 MGNMNGMNGCNAARACNATGGCNYTNGTNGAYATHCARTYNGAYCAVARGMNGTGY 1080
DB 1034 AGGGTAAAGGTAAAGACATGGCTCTAGTTCATTCAGTTCATTCATGATCAATGATGC 1093
QY 1081 GATYATATHTGYMSMSNMNGCNCNMNG 1109
DB 1094 GATYGTATCTGACGCTCAAGACCACTCG 1122

RESULT 9
US-09-540-224-3
; Sequence 3, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Glibertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; PRIOR FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-540-224-3

Query Match      64.4% Score 714.8; DB 4; Length 1472;
Best Local Similarity 52.5%; Pred. No. 6.5e-206;
Matches 582; Conservative 289; Mismatches 238; Indels 0; Gaps 0;
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QY 1 ATGCAVWNTYNAHTHTYNTAATACNTYNAHTHGYCNAAYTTTGYMSNTGYMNGAY 60
Db 93 ATGCAACGGCTCGTTTATGCTTCATCTCTGCGCGCAATAGCTGTATCCGGAC 152
QY 61 ACNWSNCGNACNCCNARMSNGCNWSNATHAAGCNYTNMNGNAAAYTNMNGN 120
Db 153 ACTTTTGCGACTCCGAGAGAGCATCATCAAGCTTTGGCAATCCCAACCTCAGAGA 212
QY 121 GAYGARSNAAYCAVYTNACNGAYTNATYMGNGAGYARACNAHTCARGTNAARGN 180
Db 213 GATGAGACATATCATCAGACTGTGACAGAGAGAGAGACATTCAGGTGACAAAC 272
QY 181 AAYGNTAYGTNCARMSNCCNMNTTYCCNAAYMSNTAYCCMNGNAAAYTNNTYNA 240
Db 273 AATGGCAATGTGAGAGTCTCTGCTCCCAACAGCTACCAAGAACTGCTTCGACA 332
QY 241 TGGMNTYTCAYWSNCRGARAAYACMGNATHCARNTYNTYGAAYACARTTYG 300
Db 333 TGGTGGCTCCGTTCCAGAGAAACACGAGATCACTGCTTCGACATCAATTCGGA 392
QY 301 YTNAGARGCNGARAAYATHTGYMNTYGAATYTGNGAGTNGARAYATHTMSN 360
Db 393 CTGAGAGACAGAAATGACATTTGTAGATGACTTGTGAAAGTTGAAAGATCTCA 452
QY 361 GARACMSNACNAATHAHTMNGMNGMTGTGYGNCAYARAGARTNCNCGMNAHT 420
Db 453 GAGAGAGCACTGTGTGAGAGAAAGATGTGTGGCCCAAGAGATCCCTCAAGATA 512
QY 421 AARMSMGAACNAAYCARATHAARATHACNTTYAARMSNGAYGATYATYTGNCAR 480
Db 513 AGCTCAAGAACAAACAGATTAATAATCAATTTAAGTGAAGTCACTGTTGTGCAAAA 572
QY 481 CCNGNTTYAARATHATYATYWSNTYNTYNGARAYTTTCARCNCGNCGNCGNSAR 540
Db 573 CCGATTCACAAATTTATTTATTCATTTGTGGAAGATTTCCACCGAAAGCCTCAG 632
QY 541 ACNAAYTGGARMSNGTNAACMSNWSNATHMSNGNNGTWSNTYAAAYMSNCGMSNGT 600
Db 633 ACCAATGGGATCAGTCAACAGCTCTTCTGCGGTGTCTTATCATCTCATCATATA 692
QY 601 ACNGAYCCNAACNTYNAHTGNGAYGNYTNAYARABATHGNCAGATTYGAYACNGT 660
Db 693 ACGGACCCCACTCTCACTGCTGATGCTCTGACCAAACTGCGCAAGATTTGATAC 752
QY 661 GARAYYNTYNAATYATYTAAYCCNGARMSNTGCGARAGAYTNGARAAATYAT 720
Db 753 GAAGATCTAATTAAGCACTTCATCAGTGTCTTGGCAAGATGATCTGGAGATTT 812
QY 721 YTNAGYACNCCMGTATMNGMNGMNSNTAYCAYGAYMNGAARMSNARGTNGAY 780
Db 813 CTGAGACCCCTCATTTATAGAGGAGGTCAATACATGATCGAAAGTCCAAAGTG 872
QY 781 GAYMNTYNAAYGAYGAYGCAABMNTAYVSNNTGYACNCCMNGNAAAYTYWSNGT 840
Db 873 GACAGGCTCATATGATGATCAAGCTTACGTTGCACTCCAGAGATCACTCTGTA 932
QY 841 AHTMNGARGRYNTAAYTYNGCAAYGTGNTTYTTCMNGNTYNTYNTYNTCAR 900
Db 933 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 992
QY 901 MANTGYGNGGNAAYTYGNGTYGNGAYGNGNATYAYGNGMNSNTGYACNTGYA 960
Db 993 CGCTGTGTGCACTGTGCTGCGGAACTGTCACTGAAAGTCTTCGACATCAAGT 1052
QY 961 GGNARAACNTNARAARATYACAGARTYNTYNTYNTYNTYNTYNTYNTYNTYNT 1020
Db 1053 GGGAGAGACAGTGAAGATATCATGAGTATTTGAAGTTGAGCTGAGCACTTCA 1112
QY 1021 MNGMNGNCGNARACNAATGCGNYTNNGAYATHTCARNTYNGAYCAYCAYGAR 1080
Db 1113 AGGGGCAACCTTAAGATATGCTCTGTGTGATATCAAGCTGATCATGAGCATGT 1172
QY 1081 GAYTGYATHTGYMSNMSNCGNCGNMG 1109
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Db 1173 GACTGTATCTGAGCTCAAGACCACTCTG 1201

RESULT 10
US-09-564-595D-52
/ Sequence 52, Application US/09564595D
/ Patent No. 6495668
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZYBFA
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/564,595D
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 09/304,216
/ PRIOR APPLICATION DATE: 1999-05-03
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 1472
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (93)...(1205)
US-09-564-595D-52

Query Match 64.4%; Score 714.8; DB 4; Length 1472;
Best Local Similarity 52.5%; Pred. No. 6.5e-206;
Matches 582; Conservative 289; Mismatches 238; Indels 0; Gaps 0;

QY 1 ATGCAVWNTYNAHTHTYNTAATACNTYNAHTHGYCNAAYTTTGYMSNTGYMNGAY 60
Db 93 ATGCAACGGCTCGTTTATGCTTCATCTCTGCGCGCAATAGCTGTATCCGGAC 152
QY 61 ACNWSNCGNACNCCNARMSNGCNWSNATHAAGCNYTNMNGNAAAYTNMNGN 120
Db 153 ACTTTTGCGACTCCGAGAGAGCATCATCAAGCTTTGGCAATCCCAACCTCAGAGA 212
QY 121 GAYGARSNAAYCAVYTNACNGAYTNATYMGNGAGYARACNAHTCARGTNAARGN 180
Db 213 GATGAGACATATCATCAGACTGTGACAGAGAGAGAGACATTCAGGTGACAAAC 272
QY 181 AAYGNTAYGTNCARMSNCCNMNTTYCCNAAYMSNTAYCCMNGNAAAYTNNTYNA 240
Db 273 AATGGCAATGTGAGAGTCTCTGCTCCCAACAGCTACCAAGAACTGCTTCGACA 332
QY 241 TGGMNTYTCAYWSNCRGARAAYACMGNATHCARNTYNTYGAAYACARTTYG 300
Db 333 TGGTGGCTCCGTTCCAGAGAAACACGAGATCACTGCTTCGACATCAATTCGGA 392
QY 301 YTNAGARGCNGARAAYATHTGYMNTYGAATYTGNGAGTNGARAYATHTMSN 360
Db 393 CTGAGAGACAGAAATGACATTTGTAGATGACTTGTGAAAGTTGAAAGATCTCA 452
QY 361 GARACMSNACNAATHAHTMNGMNGMTGTGYGNCAYARAGARTNCNCGMNAHT 420
Db 453 GAGAGAGCACTGTGTGAGAGAAAGATGTGTGGCCCAAGAGATCCCTCAAGATA 512
QY 421 AARMSMGAACNAAYCARATHAARATHACNTTYAARMSNGAYGATYATYTGNCAR 480
Db 513 AGCTCAAGAACAAACAGATTAATAATCAATTTAAGTGAAGTCACTGTTGTGCAAAA 572
QY 481 CCNGNTTYAARATHATYATYWSNTYNTYNGARAYTTTCARCNCGNCGNCGNSAR 540
Db 573 CCGATTCACAAATTTATTTATTCATTTGTGGAAGATTTCCACCGAAAGCCTCAG 632
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Qy 541 ACNAAATGGGARSNGTNAACNMSNMSNATHMSNGNGTNSMTAAAYVSNCCNMSNGTN 600
Db 633 ACCAACTGGGAATAGTCAAGAGCTCTTCTCTGGGGGTGCTCTATCACTCTCATCAATTA 692
Qy 601 ACNGAYCCNACNYTNAATGCGNAYGCTNTNGAYAAABAARATGCGAATTGAYACNGTN 660
Db 693 ACGGACCCCACTCTCACTGCTGATGCCCTGGCAAAACGTGCGAGAAATTCATATCCGCG 752
Qy 661 GARGAATYNTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 753 GAAGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 812
Qy 721 YTNGAACNCCNMGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Db 813 CTGGAACCCCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 872
Qy 781 GAYMGNNTNAAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAY 840
Db 873 GACAGGCTCAATGAAGATGTCAGAGCTTACAGTTCACCTCCAGGAATCACTCTGTAAC 932
Qy 841 ATHMGNNGARARYTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 933 CTCAAGGAGAGAGCTGAAGCTGACATGAGCTCTTCTCCAGATGCTCTCTGTCAG 992
Qy 901 MGNTEYGGNGNAAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
Db 993 CGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1052
Qy 961 GGNAAACNCTNAARATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
Db 1053 GGGAAAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
Qy 1021 MGNMGNMGNCAAAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080
Db 1113 AGGGCAAGAGCTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1172
Qy 1081 GAYTGTATGTYGWSNMSNCCNMG 1109
Db 1173 GACTGTATCTGACGCTCAAGACCACTCG 1201

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RESULT 11
US-09-808-972-3
; Sequence 3, Application US/09808972
; Patent No. 6630142
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/09/808,972
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)

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US-09-808-972-3

Query Match 64.4%; Score 714.8; DB 4; Length 1472;
 Best Local Similarity 52.5%; Pred. No. 6,5e-206;
 Matches 582; Conservative 289; Mismatches 238; Indels 0; Gaps 0;

```

Qy 1 ATGCAVMGNNTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
Db 93 ATGCAAGGCTGCTGTTAGTCTCATTTCTCTGCTGGGAACCTTAGCTGATCCGAGC 152
Qy 61 ACNMSNCCNACNCCNCAWSNCCNMSNATHAARGNNTNMGNAAYGCAAYTTNMGNGN 120
Db 153 ACTTTGGACCTCCGACAGAGCATCCATCAAGCTTTGCCGAATGCCAACCTCAGAGA 212
Qy 121 GAYGARMNAAYCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
Db 213 GATGAGACCAATCACTCAAGATTTGAACAGAGAGGAGAACATTCAGGTGCAAGC 272
Qy 181 AAYGNTAYGTCNARWSNCCNMGNTTCCNAAVMSNTAYCCNMGNAAYTNTNTNACN 240
Db 273 AATGCCATGTGCGAGAGTCTGCTCCGGAACAGCTACCCAGAGAACCTGCTTGACA 332
Qy 241 TGGMNTYTNCAVWSNCAAGARAAYACNMGATTHCARNTNTNTTYGAYAAATTTGGN 300
Db 333 TGGTGTCTCCGTTCCAGAGAAACAGGATACATGCTCTTGACCATCAATTCGGA 392
Qy 301 YTNGARARGCNAGRAAAYGATTTGTMGNATTAATTAATTAATTAATTAATTAATTAATTA 360
Db 393 CTAGAGAGAGCAAGAAATGAGATTTGAGATGATCTTTGAGAAATTTGAGAAATCTCA 452
Qy 361 GARACNMSNCAATTAATTHMGNMNGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 420
Db 453 GAGAGACACATCTGTGTGAGAGAGATGCTGTGCGCAAGAGATATCCCTCAAGATA 512
Qy 421 AARMSNMGACNAAACADATTAARATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Db 513 ACGTGAAGAACAAACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 572
Qy 481 CCNGNTTYAARATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
Db 573 CCGATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 632
Qy 541 ACNAAATGGGARSNGTNAACNMSNMSNATHMSNGNGTNSMTAAAYVSNCCNMSNGTN 600
Db 633 ACCAACTGGGAATAGTCAAGAGCTCTTCTCTGGGGGTGCTCTATCACTCTCATCAATTA 692
Qy 601 ACNGAYCCNACNYTNAATGCGNAYGCTNTNGAYAAABAARATGCGAATTGAYACNGTN 660
Db 693 ACGGACCCCACTCTCACTGCTGATGCCCTGGCAAAACGTGCGAGAAATTCATATCCGCG 752
Qy 661 GARGAATYNTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 753 GAAGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 812
Qy 721 YTNGAACNCCNMGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Db 813 CTGGAACCCCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 872
Qy 781 GAYMGNNTNAAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAY 840
Db 873 GACAGGCTCAATGAAGATGTCAGAGCTTACAGTTCACCTCCAGGAATCACTCTGTAAC 932
Qy 841 ATHMGNNGARARYTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 933 CTCAAGGAGAGCTGAAGCTGACATGAGCTCTTCTCCAGATGCTCTCTGTCAG 992
Qy 901 MGNTEYGGNGNAAATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
Db 993 CGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1052
Qy 961 GGNAAACNCTNAARATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020
Db 1053 GGGAAAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112

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EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 690
TYPE: DNA
ORGANISM: Homo sapiens
US-09-438-046-3

Query Match 36.6%; Score 406.4; DB 4; Length 690;
Best Local Similarity 55.4%; Pred. No. 1.2e-112;
Matches 332; Conservative 156; Mismatches 110; Indels 1; Gaps 1;

QY 511 GARGATTTTCACCCGAGAGCTTCAAGACCACT-GGAATCTGTCAAGAGCTCTGTT
DB 2 GAAGATTTTCACCCGAGAGCTTCAAGACCACT-GGAATCTGTCAAGAGCTCTGTT 60
QY 571 WSNNGNGTMSNTAYAAATWSNCCMSNGTNAAGAACCACTTAAATGCGATGTCNTN 630
DB 61 TCAGGATTCCTTAACTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCTG 120
QY 631 GAYABARATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 690
DB 121 GACAAAATTTGCGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 691 WSNNGCGARAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 750
DB 181 TCATGCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 751 TAYCAYGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 810
DB 241 TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 811 WSNNGYACNCCMGAAATYATWSNCCMGAAATYATWSNCCMGAAATYATWSNCCMGAA 870
DB 301 AGTTGCACTCCGAGATTTCTCGTCACTCACTCACTCACTCACTCACTCACTCACTCA 360
QY 871 GTNTTTCCTCCGAGATTTCTCGTCACTCACTCACTCACTCACTCACTCACTCACTCA 930
DB 361 GTCTTCTTTCAGATTTCTCGTCACTCACTCACTCACTCACTCACTCACTCACTCACT 420
QY 931 GTTAAATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 990
DB 421 GTCAAACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 991 YTNCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1050
DB 481 TTACGATTTGAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 1051 GAYATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1109
DB 541 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 599

RESULT 14
US-09-457-066-6
Sequence 6, Application US/09457066
Patent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1035
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
OTHER INFORMATION: 2
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (1035)
OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match 16.8%; Score 186.4; DB 4; Length 1035;
Best Local Similarity 55.6%; Pred. No. 1.2e-45;
Matches 573; Conservative 74; Mismatches 309; Indels 75; Gaps 6;

QY 82 GGNMNAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 141
DB 64 GCGARMSNAATTTTWSNCCMGAAATTTTWSNCCMGAAATTTTWSNCCMGAAATTTT 123
QY 142 GAYTTTAYMGNGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201
DB 124 CARGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 183
QY 202 MGNTTTCNAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 258
DB 184 MGNTTTCNAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
QY 259 GABAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 318
DB 244 GABAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 303
QY 319 GAYATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 378
DB 304 GAYATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 357
QY 379 MGNGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 438
DB 358 YTNNGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY 439 ATTHAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 498
DB 418 ATTHAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
QY 499 TAYMNTTNTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 558
DB 478 TAYMNTTNTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 494
QY 559 ACNMSNNAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
DB 495 NCARTTTCNAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 548
QY 619 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 678
DB 549 --NGATTTTNTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
QY 679 TTYAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 738
DB 607 YTNNGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 666
QY 739 MGNGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 792
DB 667 YTNNGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
QY 793 GAYGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 852
DB 727 GARGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 786
QY 853 YTNATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 912

Db 787 YTNARMGNAACGATGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 846
Qy 913 AATGYGNTGYGNAACGATGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 972
Db 847 AATGYGNTGYGNAACGATGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 906
Qy 973 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 1032
Db 907 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 957
Qy 1033 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 1092
Db 958 YTNCAVAAARMGNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 1017
Qy 1093 WSNMNGNCC 1103
Db 1018 MNGMNGMNAAC 1028

RESULT 15
US-09-706-968-6
Sequence 6, Application US/09706968
Patent No. 6528050
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
PRIOR FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1035
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
NAME/KEY: misc_feature
LOCATION: (1)...(1035)
OTHER INFORMATION: n = A,T,C or G
US-09-706-968-6

Query Match 16.8%; Score 186.4; DB 4; Length 1035;
Best Local Similarity 55.6%; Pred. No. 1.2e-45;
Matches 573; Conservative 74; Mismatches 309; Indels 75; Gaps 6;

Qy 82 GCNNSNATHAAGCAGTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 141
Db 64 GCNNSNATHAAGCAGTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 123
Qy 142 GAYTNTAYMNGMNGAGARACNATHCARGTNAAGGNAAGGNTAYGTNCARMSNCCN 201
Db 124 CARGAYCCNCCARCAVAGARMGNAATHAAGTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 183
Qy 202 MGNITTCNNAAYMNGTAYCCMNGNAAYTNTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 258
Db 184 MGNITTCNNAAYMNGTAYCCMNGNAAYTNTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 243
Qy 259 GABAAYACMNGNATHCARGTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 318
Db 244 GABAAYACMNGNATHCARGTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 303
Qy 319 GAYTGTGNTAYGAYTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 378

Db 304 GAYTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 357
Qy 379 MNGMNGMNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 438
Db 358 YTNMNGMNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 417
Qy 439 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 498
Db 418 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 477
Qy 499 TAYMNTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 558
Db 478 TAYMNTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 549
Qy 559 ACNMSNATHAAGCAGTGTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 618
Db 495 NCARTTAYACNAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 548
Qy 619 GCNNGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 678
Db 549 --NGAYTNTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 606
Qy 679 TTYAAYCCNAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 738
Db 607 YTNARMGNAACGATGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 666
Qy 739 MNGMNGMNTAYCAGAYMG-----NABMSNABRTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 792
Db 667 YTNMNGMNTAYCAGAYMG-----NABMSNABRTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 726
Qy 793 GAYGAYCCNABRTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 852
Db 727 GARGRTMNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 786
Qy 853 YTNABRTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 912
Db 787 YTNABRTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 846
Qy 913 AATGYGNTGYGNAACGATGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 972
Db 847 AATGYGNTGYGNAACGATGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 906
Qy 973 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 1032
Db 907 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 957
Qy 1033 AABAARTAYCAGARGTNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 1092
Db 958 YTNCAVAAARMGNTGATGTCGCGGNGTGYTNTGTNNAARMGNTGYGNGN 1017
Qy 1093 WSNMNGNCC 1103
Db 1018 MNGMNGMNAAC 1028

Search completed: November 15, 2004, 20:18:43
Job time : 146.177 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 18:05:02 ; Search time 3227.52 Seconds
(without alignments)
1857.496 Million cell updates/sec

Title: US-09-876-813-6

Perfect score: 1110

Sequence: 1 atgcaagmnygnahcttctgc.....gyenwbnmgnmcncmgn 1110

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798	71.9	1110	11	US-09-876-813-6
2	798	71.9	1828	15	US-10-011-864-3
3	798	71.9	1828	15	US-10-041-860-50
4	798	71.9	1829	16	US-10-321-962-3
5	798	71.9	1882	9	US-09-808-972-1
6	798	71.9	1882	11	US-09-876-813-1
7	798	71.9	1882	13	US-10-139-583-36
8	798	71.9	1882	13	US-10-039-847A-1
9	798	71.9	1882	15	US-10-226-559-1
10	798	71.9	1882	15	US-10-274-638-1
11	798	71.9	1882	15	US-10-365-095-1
12	798	71.9	1882	16	US-10-606-055-1

13	798	71.9	2253	13	US-10-086-623-7	Sequence 7, Appli
14	798	71.9	2253	14	US-10-260-539-7	Sequence 7, Appli
15	798	71.9	2253	15	US-10-246-091-4	Sequence 4, Appli
16	798	71.9	3736	15	US-10-258-557-1	Sequence 1, Appli
17	798	71.9	3739	17	US-10-650-284-1	Sequence 1, Appli
18	798	71.9	3798	9	US-09-915-562-17	Sequence 17, Appli
19	798	71.9	3798	15	US-10-277-802-17	Sequence 17, Appli
20	797.6	71.9	4001	9	US-09-915-582-35	Sequence 35, Appli
21	797.6	71.9	4001	15	US-10-277-802-35	Sequence 35, Appli
22	757.4	68.2	1162	14	US-10-028-072-185	Sequence 185, App
23	757.4	68.2	1162	14	US-10-140-808-185	Sequence 185, App
24	757.4	68.2	1162	14	US-10-121-049-185	Sequence 185, App
25	757.4	68.2	1162	14	US-10-123-004-185	Sequence 185, App
26	757.4	68.2	1162	14	US-10-140-470-185	Sequence 185, App
27	757.4	68.2	1162	14	US-10-175-746-185	Sequence 185, App
28	757.4	68.2	1162	14	US-10-176-918-185	Sequence 185, App
29	757.4	68.2	1162	14	US-10-176-921-185	Sequence 185, App
30	757.4	68.2	1162	14	US-10-137-865-185	Sequence 185, App
31	757.4	68.2	1162	14	US-10-140-474-185	Sequence 185, App
32	757.4	68.2	1162	14	US-10-142-431-185	Sequence 185, App
33	757.4	68.2	1162	14	US-10-143-114-185	Sequence 185, App
34	757.4	68.2	1162	14	US-10-140-002-185	Sequence 185, App
35	757.4	68.2	1162	14	US-10-142-419-185	Sequence 185, App
36	757.4	68.2	1162	14	US-10-123-262-185	Sequence 185, App
37	757.4	68.2	1162	14	US-10-142-423-185	Sequence 185, App
38	757.4	68.2	1162	14	US-10-121-050-185	Sequence 185, App
39	757.4	68.2	1162	14	US-10-141-755-185	Sequence 185, App
40	757.4	68.2	1162	14	US-10-143-032-185	Sequence 185, App
41	757.4	68.2	1162	14	US-10-123-108-185	Sequence 185, App
42	757.4	68.2	1162	14	US-10-123-236-185	Sequence 185, App
43	757.4	68.2	1162	14	US-10-123-261-185	Sequence 185, App
44	757.4	68.2	1162	14	US-10-140-921-185	Sequence 185, App
45	757.4	68.2	1162	14	US-10-140-928-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-09-876-813-6
; Sequence 6, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles B.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZWEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876, 813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564, 595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304, 216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164, 463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180, 169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-813-6
Query Match 71.9%; Score 798; DB 11; Length 1110;


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Db      602 AAATCAGAAAGCAACCAATTBAAATCACAATTCAAGTCCGATGACTCTTTGTGGCTTAAA 661
Qy      481 CCNGGNTTAAATATHTAATTAAYWSNTYNTYNGARGAYTTYCARCCNGCNGCNGCNGMSNGAR 540
Db      662 CTTGGAATTCAGAGATTATATATTCTTTGTGCGAAGATTTCCAAACCCGACGACGCTTCAAG 721
Qy      541 ACNAAATYTGGAARWSNGTNAACNWSMNSNAATHMSNGNGNTNWSNTAYAAATWSNCNWSNGTN 600
Db      722 ACCAATCTGGGAATCTGTGACAAGCTCTATTTCACAGGGGATATCTTAATACCTCCACAGTA 781
Qy      601 ACNGAYCCNACNATYNAATHGNCNGAYGCAANTNGAYTAABAATGNCGARFTTYGAYCNGTN 660
Db      782 ACCGATCCCACTCTATATGCGGATCTCTTGACACAAAATAATTCAGAAATTTGATGATCAGTG 841
Qy      661 GARGAYTNTYNTAARTAYTAYTYAAAYCCNGARWSNNTGGCARGARAYTNGABAAVAATGTAY 720
Db      842 GAAAGTCTGCTCAAGTACTTCAATCAGAGTCATGCGCAAGAAGATCTTGAGAAATATGTAT 901
Qy      721 YTNNGAYACNCCMGTATYMGNGNNGMSNTAYCAAYGAYMGNAAARWSNAARCTNGAYTTN 780
Db      902 CTGGAACACCCCTCGGTATCGAGGCAAGCTCATACCATGACCGGAGTCAAAAGTTGACCTG 961
Qy      781 GAYMGNNTYNTAAYGAAYGACNAAABMGNATPYMSNTGYACNCCMGNAAATAYAWSNNTNAY 840
Db      962 GATYMGCTCAATGATGATGACCAAGGCTTACAGTTCACCTCCACGAAATTAATCTCGGTCAAT 1021
Qy      841 ATTHMNGARGARYTNAARYTYNGCNAAAYGTNGTNTTYTYCCNMGTGYTYNTYNGTNGAR 900
Db      1022 ATTAAGAGAAGAGCTGAATGATGGCCAAATGTGGCTTTCCACGTTGGCTCCTCGTGAG 1081
Qy      901 MGNTRYGNGNGNAAYTYGANTGYGGAACNGTNAAYTYGGMNWSNTGYACNTGYAAYWSN 960
Db      1082 CGCTGTGAGGAAATTTGTGGCTGTGGAATCTGTCAACTGAGAGCTCTGCAACATGCAATTC 1141
Qy      961 GGNABAACNGTNAABAARTAYCAGABGNNTYNCARTTYGARCCNGNCAVATTAABGN 1022
Db      1142 GGGAAACCGTGAAAAAGATCATATAGGATTAACGTTGAGCTGGGCAACATCAAGAG 1201
Qy      1021 MGNNGMNGNCAAPACNATGACNATYNGCANTYNGAYTHCARTYTNGAYCAYCAYGARBMNTGY 1080
Db      1202 AGGGGTAAAGCTAAGACCAATGCTCTAATGTGACATCCAGTTGATCAACCATGAAGATGT 1261
Qy      1081 GAYTGATHTGYWSMNSMNGCNCNMG 1109
Db      1262 GATTGTATCTGCACTCAAGACCACTCG 1290

RESULT 3
US-10-041-860-50
; Sequence 50, Application US/10041860
; Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvahan, Jose R.F.
APPLICANT: Xia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezeber, Binuam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
FILE REFERENCE: THEREOF
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 1828
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-50

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Query Match	71.9%;	Score 798;	DB 15;	Length 1828;
Best Local Similarity	56.4%;	Pred. No. 2.8e-202;		
Matches 626;	Conservative 300;	Mismatches 183;	Indels 0;	Gaps 0;

QY	1	ATGAYMGNNTNAATHTTGTGTTAAACNTYNTATHGVCNAAATYTTGWSNTVMGNNGAY	60
Db	182	ATGCACCGGCTCATCTTGTGTCTACACTTAATCTGCGAATCTTTTGGACGCTGTGGGAC	241
QY	61	ACNWSNCGNACCCNCAWNSNCGNWSNATHAARGCNTYTMGNAAAYCNAAAYTTNMGNGN	120
Db	242	ACTTCTGCACACCCGACAGAGCGCATCTCATCAAGCTTTGGCCACAGCCCAACTCTCAGGCA	301
QY	121	GAYGARMSNAAAYCAAYTNACNGAYYTNTNAYMGNMNGAYGABACNATHCAGSTNABRGN	180
Db	302	GATGAGACCAATCTACCTCAGACTTGTACCGAAGATGAGACCATCCAGGTGAAGAAGA	361
QY	181	AAYGANTYVGNRCARWSNCCNMGNNTYCCNAAYSNNTAYCCNMGNAAAYTYNTYNTNACN	240
Db	362	AAAGCTACGTGCAGAGCTCTAGATCTCCGAAACAGCTACCCAGGAACCTGCTCTGACAC	421
QY	241	TGSMGNTYTNCAYSWNCARABAPAYACNMGNATHCARVYNTGNTTYGAYAAACATPTTGGN	300
Db	422	TGGCGGCTTCACCTCTCAGAGAAATCAACGAGTACAGTACGTGTTGACATCAGTTTGGAA	481
QY	301	YTNAGARGGONGAPAAAYGAYATHGVMGNATAYGAYTYTGNMGAGSTNGARGAYATHMSN	360
Db	482	TTAGAGGAGAGAAATGATATCTGTAAGTATGATTTTGTGGAAAGTTGAAATATATATCC	541
QY	361	GABACMSNACNATHATMGNGNMGNNGTGTGCGNCAVYARGAGTNCNCCNMGNATH	420
Db	542	GAAACAGTACATTAATTATAGAGAGACGATGCTGTGACACAAAGAGTTCTCTCAAGATNA	601
QY	421	AARBSNMGNACNAAVCAATATAPATACNTTYAARBSNGAYATYATTYTGNCNAR	480
Db	602	AAATCAAGAAAGAAACCAATTAATAATCACTTCAAGTCCGATGACTCTTGTGTGCTAA	661
QY	481	CCNGNTTYABATHATATAYMSNTYNTYNGARGVTTYCARCCNGCNGCNGSNNGAR	540
Db	662	CTGGATTCAGATTTATATATATCTTCTTGTGGAAGATTCACACCCGACAGCTTCAGAG	721
QY	541	ACNAAVTGGGARSWSNGTNACNWSMWSNATHMSNGNNGTMSNTAYAAYSNCCNMSNGTN	600
Db	722	ACCAACTGGGATCTGTCACAAGCTCTATTTCAAGGAGTATCTTAATACCTCTCATCAGTA	781
QY	601	ACNNGAYCCNACNTYNTATHGNCNGAYGCNTYNGAYAPARAPATHGCGARTTYGAYACNGTN	660
Db	782	ACGGATCCCACTCTGATGCGGATGCTCTGCGACAAAATAATYGCAAAATTTGATATCAGTG	841
QY	661	GARGAYYNTYNTAARATATYTTAAVYCNABRMSNTGGCARGARGAYYTNGABAAVATGTAY	720
Db	842	GABGATCTGCTCAAGTACTTCAATCAAGATCATGCGAAGAGATCTTGAAGATATGTAT	901
QY	721	YTNGAAYACNCCNMGNATYMGNGNMMSNNTAYCAVGYMGNAPARMSNABRTNGAYYTN	780
Db	902	CTGGACACCCCTCGGTATCGAGGACGATACATACATGACCGGAAATCAAAAGTGAACCTG	961
QY	781	GATMGNNTNAAVGAAYGVCNABRMGNATYMSNTGYACNCCNMGNAAATYAYNSNGTNAAY	840
Db	962	GATAGGCTCAATGATGATGCCAAGGCTTACAGTTGCACTCCACGAAATTAATCTCGGTCAAT	1021
QY	841	ATHMGNARGARYNTNAAAYTYNGCNAAVGTNGNTNTTYTTCNMGNGTGYTYNTYNTGNCAR	900
Db	1022	ATTAAGAGNAGCTGABAGTTGGCCAAATGTGTTCTTTTCCACGTTGGCTCTCTCGTGACG	1081
QY	901	MGNTRYGNGNAAAYTGAGNTGYGABACNGTNAAYTGAMGNSTGYACNTGYAAYSN	960
Db	1082	CGCTGTGAGGAAATYTGCGTGTGGAACGTGCACATCGAAGGTCTCTGACACATGCAATTCA	1141
QY	961	GGNABACNNTNABAAATATCAVABRTYNTNCAATTYTGARCCNGNCAATYTHABRGN	1022
Db	1142	GGGAAAAACCGTGAAGAAATATCATAGGATATTAACGTTTGAGCCTGGGCCACATYCAAGG	1201

QY	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608
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RESULT 4

```

US-10-321-962-3
/ Sequence 3, Application US/10321962
/ Publication No. US20040006015A1
/ GENERAL INFORMATION:
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Fernandes, Elma
/ APPLICANT: Jeffers, Michael E.
/ APPLICANT: Larocheille, William J.
/ APPLICANT: Lichenstein, Henry S.
/ APPLICANT: Peterson, Jeffrey
/ APPLICANT: Prayaga, Sudhirdas
/ APPLICANT: Ritman, Beth
/ APPLICANT: Shimkets, Juliette
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Yang, Meljia
/ APPLICANT: Curagen Corporation
/ TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
/ TITLE OF INVENTION: Treatment of Inflammatory Bowel Disease
/ FILE REFERENCE: 15966-5574 IBD CIP2
/ CURRENT APPLICATION NUMBER: US/10/321,962
/ CURRENT FILING DATE: 2002-12-16
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: Cursaseq1st version 0.1
/ SEQ ID NO 3
/ LENGTH: 1829
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (183) .. (1292)
/ US-10-321-962-3

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Query Match	71.9%	Score 798	DB 16	Length 1829
Best Local Similarity	56.4%	Pred. No. 2.8e-202		
Matches 626	Conservative 300	Mismatches 183	Indels 0	Gaps 0

Qy	1	ATGAYMGNNTNAHTHTTGGNTTAACNYNTNAHTHTGCAAAATTTGTWSTGTMNGAY	60
	183	ATGACCGGGCTCATCTTTGTCTACACTTCAACTGTGGCAACTTTTGGACGCTGTGGGAC	242
Qy	61	ACNWSNCAACNCCNBARMSNCGMSNATHAARGCNYNMGAAAGCAAAATYTMGMN	120
Db	243	ACTTCTGCAACCCCGAGAGCGCATCAATCAAAAGCTTTGGCGAAGCCMACTTAGCGCA	302
Qy	121	GAYGARMSNAAYCAAYTNAACGAYTNTAYMGNGAYAGARACATTCAGTNAARGN	180
Db	303	GATGAGAGCAATACCTTCACAGACTGTACCAAGAGATGAGACCATCCAGGTAAAGGA	362
Qy	181	AAYGANTAYGTCNARMSNCCMNGTTCNAAWMSNTAYCCMGNAAAYTNTYNTACN	240
Db	363	AACGGCTACGTGACAGTCTGTGATTTCCGGAACACTACCCAGAACCTGCTCTTACA	422
Qy	241	TGCMGNTYNTCAWNSNCARGAAPAAVACNMGNAATHCARNTYNTNTTGYAAAYCAATTYGN	300
Db	423	TGCGCGCTTCACCTCAGGAGAAATACAGGATACAGTAGTGTGACAACTAGTTTGA	482
Qy	301	YTMGARGAGCNCARGAAYAYATHHTGNGNTAYGAYTTGTNGARGTNGARGAYATHWSN	360
Db	483	YTAGAGGAAGCCGAPAAATATGATCTGTAGTATGATTTTGTGAAGTTGAAGATATTC	542
Qy	361	GABACWSNAACNATHTHMGNGMNGTGTGTGNCAYARARGRTNCCNCCMGNATC	420

Db	543	GAACACAGTACCATTTATTAGAGAGAGATGRTGTGGACACAAAGAAATTCCTCCAGAGATA	602
Qy	421	AAATSMGMAACNAATCARTTAARATTAACNTTAAATSMNGAYGYATYATTTGTGNCMAAR	480
Db	603	AAATCAAGAACCAAAATTTAAATTCACATTCCAAGTCCGATGACTCTTTGTGGCTTAA	662
Qy	481	CCGAGTTTAAABATHTAATAYMSNTYNTNBARAYTTTCARCCNGCNGCNGCMSGAR	540
Db	663	CTGGAGTTCAAGATTTAATTTATCTTTGGTGGAAGATTTCCAAACCCGAGACGTTCAAG	722
Qy	541	ACNAATYGGAGATSMNGTNAACNWSMNSNTATHSNNGSNGTNNSTNTAYAAVMSNCCMSNGT	600
Db	723	ACCAATCTGGGAATCTGTGACAAAGCTCTATTTCCAGGGTATCTCTTAATCTCCATCAGTA	782
Qy	601	ACNGAYCCNACNYNTAATGCGNGAYGCVYTNGVAAVARAATHTGCGARTTYGAYACNGTN	660
Db	783	ACCGATCCCACTCTGATTTGGGAGTGTCTGGACAAAAAAATTTGAGAAATTTGATACGTG	842
Qy	661	GARGAYTNTYNTAATATTTTAAATCCNGARHSNTGCGARBARAYTTNGARAATGTATY	720
Db	843	GAAGATCTGTCTCAAGTACTTCAATTCAGAGTCCAGAGTCAAGGACGAGAMAGATCTTGAGAAATATGAT	902
Qy	721	YTNCAVACNCCMGNTATVMGNGMGMWSNTAYCAYAYGNAARMSNABRGNTGAYTN	780
Db	903	CTCGACACCCCTCGGTATCGAGGCGAGCTCATACATACCGGAAGTCAAAAGTTGACCTG	962
Qy	781	GAVMGNTMAAYGAYGAYGACNAABMGNTAYMSNTGYACNCCMMGNAATYAYMSNGTMAAY	840
Db	963	GATAGGTCATATGATGATGCGCAACGTTACAGTTGACCTCCAGGAATTTACTCGGTCAAT	1022
Qy	841	ATTHMNGARGARYTMAARYTNGCMAAYGTNGTNTTTTTCMNGTGYTNTYTNGTNCAR	900
Db	1023	ATPAAGAGAAGCTGGAAGTTGGCCAAATGTGTCTTCTTTCACAGTTGCCCTCTCGTGACAG	1082
Qy	901	MGNTYGGNGGNAAYTGTGNTGTGAGNACNGTMAAYTGGMGMSNTGYACNTGYAAVMSN	960
Db	1083	CCCTGTGAGGAATAATGTGGCTGTGGAACCTGTCACTGGAGGCTCTGCAACATGCAATTTCA	1142
Qy	961	GSNAARACNGTMAARAAATYACAYGARGTYTNCARTTYGARCCNGMNCAYATTAABMGN	1020
Db	1143	GGGAAAAACGTAAGAAAAGTATCATGAGGTATTCAGTTTGAAGCTGGCCACATCAAGAGG	1202
Qy	1021	MNGMNGMNGCMAARCAATGCGCNYTNGTNGAYATHTCARAYTNGAYCAYAYABRMNGTY	1080
Db	1203	AGGGGTATAGCTTAAGACCAATGGCTCTTAGTTGACATCCAGTTGATCAACATGAACGATGT	1262
Qy	1081	GAYTGYATHTGYSMSNMGNCNCCMMG	1109
Db	1263	GATTTATCTGACACTCAAGACCACTTCG	1291

RESULT 5

US-09-808-972-1
Sequence 1, Application US/09808972
Patent No. US20020064832A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Topouzis, Stavros
APPLICANT: Gilbertson, Debora G.
TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 00-79
CURRENT APPLICATION NUMBER: US/09/808,972
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/235,295
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/132,250

PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1882
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (226)...(1338)
US-09-808-972-1

Query Match 71.9%; Score 798; DB 9; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAVMGNVNTAHTTGTATVACNTNATHTGVCNAAVYTYGWSNTGYNGAY 60
DB 226 ATGCAACCGGCTCATCTTGTCTACACTCTAATCTCGCAAACTTTTGACGCTGTGGGAC 285
QY 61 ACNMSGNCNACNCNARMSNCGNMSNATTHARGCNTNMGNAAVGCNAAVYTNMNGN 120
DB 286 ACTTCTGCAACCCGCGACGAGCATCCATCAAAAGCTTTGGCGCAACGCAACCTCAGGCA 345
QY 121 GAYGARMSNAAYCAVYTNACNGAYVYTNAYMNGMNGAYGARACNATHCARGTNAARGN 180
DB 346 GATGAGACCAATCACTCAGACACTTGTACCAAGATGAGATGACATCCAGGTGAAGA 405
QY 181 AAYGNTAYGTNCARMSNCGNMTTYCCNAAVMSNTAYCCNMGNAAYVYTNACN 240
DB 406 AACGGCTACGTCAGAGCTCTAGATTCCGAAACACTACCCAGGAACCTGCTCTGACA 465
QY 241 TGGMNTNCAVMSNCARGAABAAYCNMGNAATHCARYNTNTTYGAAVACARTTYGN 300
DB 466 TGGGGCTTCTCTCAGAGAAATACGAGATACAGTAGTGTGGACAAATCAGTTTGA 525
QY 301 YTNARGARGGNCARAAVAYATHTGYMNTAYGAYVYTYGNTGARGTNGARGAYATHMSN 360
DB 526 TTAAAGAGAGCAAAATGATATCTGTAGCTTGTGAGTTTGTGGAAGTTGAATATACC 585
QY 361 GARACNMSNACNATHATMGNGMNGNTGGTGYGNCAYVARGATNCCNCGNNAATH 420
DB 586 GAAACAGTACCATATTAGAGAGCATGTGTGACAAAGAAAGTTCTCTCAAGATTA 645
QY 421 AARMSNMGNAAYCAATTHAATHACNTTYAARMSNGAYATATYTYGNCNAR 480
DB 646 AAATCAAGAACGAACCAATTAATAATCAATTCAGACTCGACTTGTGTAA 705
QY 481 CCGNGNTTYAARATHTATAYVSNYTNNGARGAYTYTCARCCNGCNGCNGNNGAR 540
DB 706 CTTGATTCAGAGTTATATATCTTCTGGAAGATTTCCAAACCGCAGCAGCTTCAAG 765
QY 541 ACNAAVYTGGAWSNGTNAACNMSNNAATHMSNGNGTWSNTAYAAVMSNCGN 600
DB 766 ACCAATCGGAGATCTGTCAAGACTCTATTTCAGGGGTATCTATTAATCTCCATCAGTA 825
QY 601 ACNAYCCNACNNTAHTGNCAGYCNNTNGAYVAAARATHTGNCATTYGAYACN 660
DB 826 ACGGATCCACTCTGATTCGAGTCTGTGACAAAATTTGCAAAATTTGATCACTG 885
QY 661 GARGAYVYTNAAATATYTAAYCCNGARMSNTGCGARGAGAYTNGARAAYATGAY 720
DB 886 GAAATCTGCTCAAGTACTTCAATCCAGATCATGCGAAGAGATCTTGAGAAATATAT 945
QY 721 YTNAGYACNCCNMTAYMNGMNGMNSNTAYCAVYAGMNAARMSNAARNTGAY 780
DB 946 CTGGAACCCCTCGGTATCGAGGAGGTCACTACATGACCGGAAGTCAAAAGTTGACCTG 1005
QY 781 GAYMNTNAAVAGAYGACNAAARMSNTAYVSNNTYACNCCNMGNAATATYVSN 840
DB 1006 GATAGGCTCAATGATGACCAAGGTTACAGTTTCACTCCAGGAATTTCTCGGTCAAT 1065
QY 841 ATHMGNGARGAYTAAYTNGCNAAVGTNGTNTTYTTCNMGNTGYVYTNGTNCAR 900

DB 1066 ATAAAGAGAGCTGAAGTGGCCAAATGTGCTCTTCTTCCACGTTGCTCCTCGTGAG 1125
QY 901 MGNVYCGNNGNAAVYTGATNGYGNACNCTNAAVYTGCMGWSNTGYACNMGVAAVSN 960
DB 1126 CGCTGTGAGAAATTTGGCTGTGAACCTGTCAACTGAGGTCTGTGACATGAATTTCA 1185
QY 961 GGNABACNNTNAAARATAYCAVARGTNTNCAATTYGARCCNGCNGCAVATHAARMGN 1020
DB 1186 GCGAAACCGTGAAAGATATCATGAGTATTTACAGTTTGAGCCCTGGCAGATCAAGAG 1245
QY 1021 MNGNMGNGNABACNATGCGVYTNNGAYVATHCARYTNAGVAYCAVARGMNTGY 1080
DB 1246 AGGGGTAGAGCTTAAGACCATGGCTCTAGTTGACATCCAGTTGATCCACATGAACGATGC 1305
QY 1081 GATGYATHTGYWSNMSNMGNCNCGNG 1109
DB 1306 GATGTATCTGCAAGCTCAAGCAACCTCG 1334

RESULT 6

US-09-876-813-1

; Sequence 1, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVBSF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876, 813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564, 595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304, 216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164, 463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180, 169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-09-876-813-1

Query Match 71.9%; Score 798; DB 11; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAVMGNVNTAHTTGTATVACNTNATHTGVCNAAVYTYGWSNTGYNGAY 60
DB 226 ATGCAACCGGCTCATCTTGTCTACACTCTAATCTCGCAAACTTTTGACGCTGTGGGAC 285
QY 61 ACNMSGNCNACNCNARMSNCGNMSNATTHARGCNTNMGNAAVGCNAAVYTNMNGN 120
DB 286 ACTTCTGCAACCCGCGACGAGCATCCATCAAAAGCTTTGGCGCAACGCAACCTCAGGCA 345
QY 121 GAYGARMSNAAYCAVYTNACNGAYVYTNAYMNGMNGAYGARACNATHCARGTNAARGN 180
DB 346 GATGAGACCAATCACTCAGACACTTGTACCAAGATGAGATGACATCCAGGTGAAGA 405
QY 181 AAYGNTAYGTNCARMSNCGNMTTYCCNAAVMSNTAYCCNMGNAAYVYTNACN 240
DB 406 AACGGCTACGTCAGAGCTCTAGATTCCGAAACACTACCCAGGAACCTGCTCTGACA 465
QY 241 TGGMNTNCAVMSNCARGAABAAYCNMGNAATHCARYNTNTTYGAAVACARTTYGN 300

Db 466 TGGCGCTTCACTCTCAGAGAAATACAGATACAGCTAGTGTTCATCAATCAGTTTGA 525
 Qy 301 YTNAGARGCNGARAAAYGATHTGTGNTAYGATTTGTNGARGTNGARAYATHMSN 360
 Db 526 TTAGAGGAGCAGAAATATATCTTCTAGCTATGATTTGTGAGAGTTGAAGATTAATCC 585
 Qy 361 GABACMSNAATHTATHMNGNMGNTGTGTGNCAYARAGRTNCCNMGNAATH 420
 Db 586 GAACCGATACCTATTATAGAGCAGATGTGTGACACAGAGAGTTCTCCAGAGATA 645
 Qy 421 AARMSMGNAATGABATHTAARATHACNTTAAARMSAGATTAATTTGTNGCNAR 480
 Db 646 AATCAAGAACGAAACCAATTAATAATCAATTCAGATTCGAGACTTCTTGTGTAA 705
 Qy 481 CCNGNTTAAATHTATAYATWMSNTYNTNGARGATTTCAACGNCNGCNGCNSNGAR 540
 Db 706 CTTGATTCAGATTTATATTCTTGTGGAAGATTTCCACCCGACAGCTTCAAGG 765
 Qy 541 ACNAATYGGARMSNGTNAACMSNMSNATHMSNGNTWSTAYAAVMSNCNMSNGTN 600
 Db 766 ACCAATCGGAATCTGTCAAGACTTATTTCAAGGGGTATCTTATACCTTCATCAGTA 825
 Qy 601 ACNGAYCCNACNTYNAHTGNCNGAYGNTNGAYAAARABATHTGNCARTTYGAYACNTN 660
 Db 826 ACGGATCCCATCTGTATTCGAGATCTCTGACAAAAAATTTGCAAGATTTGATACAGTG 885
 Qy 661 GARGAYTNTYNAARTAYTTVAAYCNGARMSNTGCGARGARAYTNGARAAVATGAY 720
 Db 886 GAAGATCTGTCTCAAGTCTTCAATCCAGGTCATGCGAAGAAAGATCTTGAGATATGTAT 945
 Qy 721 YTNAGAYACNCCMGNTAYMNGNGNMSNTAYCAVAYMNGNAARMSNAGTNGAYTN 780
 Db 946 CTGACACCCCTCGGTATCGAGGCGATACATACATACCGAAGTCAAAAAGTTGACCTG 1005
 Qy 781 GAYMNTYNAAYGAYGAYCNAARMSNTAYMNTGAYACNCCMGNAATTAAYMNGTNAAY 840
 Db 1006 GATAGGCTCAATGATGATGCCAAGGTTACAGTTGCACTCCAGAGATTAATCTCGTCAAT 1065
 Qy 841 ATTHMNGARGARYTNAAYTNGCNAAYTNGTNTTCTTCCNMGNTYNTYNTNGTNCAR 900
 Db 1066 ATAAGAGAGAGCTGAGAGTGTGCGCAATGTGTCTTCTTCCAGCTTGTGCTCGTGCAG 1125
 Qy 901 MNTGTGNGNAAAYTGTGNTGTGNGNACNGTNAAYTGGMNMGNTGACNTGAAVMSN 960
 Db 1126 CGCTGTGAGAGAAATTTGCTGTGGAATCTGCACTGAGAGTCTCTGACATGCAATTC 1185
 Qy 961 GGNARACNGTNAARATAYCAYGARGTNTGARTTYGARGCNGNCAVATHAAMGN 1020
 Db 1186 GGGAAACCGTGAAAAAGTATCATGAGGTATTACAGTTGAGCTGCGCACATCAAGG 1245
 Qy 1021 MNGNMGNGNARACNAHTGNTGTNGAYATHCARNTNGAYCAVAGARMNTGY 1080
 Db 1246 AGGGGTAGAGCTAAGACCATGTGCTGTGATCAATTCAGTTGATCAATGAAAGTATGC 1305
 Qy 1081 GAYTGYATHTGYSMWSMNGCNCNMG 1109
 Db 1306 GATTGTATCTGACCTCAAGACCACTCG 1334

RESULT 7
 US-10-139-583-36
 ; Sequence 36, Application US/10139583
 ; Publication No. US20020177193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Shoemaker, Kimberly E.
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: West, James W.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
 ; FILE REFERENCE: 98-60

; CURRENT APPLICATION NUMBER: US/10/139, 583
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 09/457, 066
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 36
 ; LENGTH: 1882
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (226)...(1338)
 US-10-139-583-36

Query Match 71.9%; Score 798; DB 13; Length 1882;
 Best Local Similarity 56.4%; Pred. No. 2,9e-202;
 Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

Qy 1 ATGCAAGNTYNAATHTTGTNTAYACNTYNAHTGNCNAAYTTTGTGMSNTGMYNGAY 60
 Db 226 ATGCAAGGCTCATCTTGTCTACACTTAATCTGCGAAACTTTGCACTGTGCGGAC 285
 Qy 61 ACMSNCGNACNCCNARMSNGNMSNATHARAGCYTNGNNAAYGNAAYTNGMNGN 120
 Db 286 ACTTCTGCAACCCGCGAGAGCGATCATCAAGCTTTGGCAACGCCAATCTCAGCGCA 345
 Qy 121 GARGARMSNAAYCAVYTNACNGAYTNTAYMNGNGAYARACNATHCARNTAARGN 180
 Db 346 GARGAGCAATCACTCAAGACTTGTACCGAAGAGATGACATCCAGGTGAAGA 405
 Qy 181 AAYGNTAYGTNCAARMSNCCNMGNTTCCNAAYMSNTAYCCNMGNAAYYNTYNTNACN 240
 Db 406 AACGGTACGTGAGAGTCTTATATTCGGAACGCTACCCAGGAATCTGCTCGACA 465
 Qy 241 TGGMNTYNAAYSNARBARAAVACNMGNAHTCARNTGNTTYGAYAAVCAATTYGN 300
 Db 466 TGGCGCTTCACTCTCAGAGAAATACAGATACAGCTAGTGTTCATCAATCAGTTTGA 525
 Qy 301 YTNAGARGCNGARAAAYGATHTGTGNTAYGATTTGTNGARGTNGARAYATHMSN 360
 Db 526 TTAGAGGAGCAGAAATATATCTTCTAGCTATGATTTGTGAGAGTTGAAGATTAATCC 585
 Qy 361 GABACMSNAATHTATHMNGNMGNTGTGTGNCAYARAGRTNCCNMGNAATH 420
 Db 586 GAACCGATACCTATTATAGAGCAGATGTGTGACACAGAGAGTTCTCCAGAGATA 645
 Qy 421 AARMSMGNAATGABATHTAARATHACNTTAAARMSAGATTAATTTGTNGCNAR 480
 Db 646 AATCAAGAACGAAACCAATTAATAATCAATTCAGATTCGAGACTTCTTGTGTAA 705
 Qy 481 CCNGNTTAAATHTATAYATWMSNTYNTNGARGATTTCAACGNCNGCNGCNSNGAR 540
 Db 706 CTTGATTCAGATTTATATTCTTGTGGAAGATTTCCACCCGACAGCTTCAAGG 765
 Qy 541 ACNAATYGGARMSNGTNAACMSNMSNATHMSNGNTWSTAYAAVMSNCNMSNGTN 600
 Db 766 ACCAATCGGAATCTGTCAAGACTTATTTCAAGGGGTATCTTATACCTTCATCAGTA 825
 Qy 601 ACNGAYCCNACNTYNAHTGNCNGAYGNTNGAYAAARABATHTGNCARTTYGAYACNTN 660
 Db 826 ACGGATCCCATCTGTATTCGAGATCTCTGACAAAAAATTTGCAAGATTTGATACAGTG 885
 Qy 661 GARGAYTNTYNAARTAYTTVAAYCNGARMSNTGCGARGARAYTNGARAAVATGAY 720
 Db 886 GAAGATCTGTCTCAAGTCTTCAATCCAGGTCATGCGAAGAAAGATCTTGAGATATGTAT 945
 Qy 721 YTNAGAYACNCCMGNTAYMNGNGNMSNTAYCAVAYMNGNAARMSNAGTNGAYTN 780
 Db 946 CTGACACCCCTCGGTATCGAGGCGATACATACATACCGAAGTCAAAAAGTTGACCTG 1005
 Qy 781 GAYMNTYNAAYGAYGAYCNAARMSNTAYMNTGAYACNCCMGNAATTAAYMNGTNAAY 840

Db 1006 GATAGCTCATATGATGATGCCAAGCTTACAGTTGCACTCCACAGAAATTACTCGTCAAT 1065
Qy 841 ATTHMGARGARATYNTAATYNTGNAAYATGNTGNTTATYTCNMGNTGYNTYNTGNTCAR 900
Db 1066 ATTAAGAGAGAGCTGAGTGGCAATGTGCTTCTTCCATGCTTCCAGTGGCTGCTGTCAG 1125
Qy 901 MGNTRYGNGNGNAAYTGYGNTGYGNAACNGTNAAYTGMGMSNTGYACTGYAAVYSN 960
Db 1126 CGCTGTGAGAGAAATGTGGCTGTGGAACCTGCACTGAGAGTCTGTCACATGCAATTC 1185
Qy 961 GGNABACNGTNAABARTAYCAYGARTYNTGARTYTCARCCNGNCAYATTAARMGN 1020
Db 1186 GGGGAAACCGTGAAGAAATGATCATGAGGTATTAACAGTTGAGCTGGCCATCATCAAGAG 1245
Qy 1021 MNGNGMNGCNAARACATGCGVNTGNTGNAAYATHTCARNTGNAAYCAYGABMGNTGY 1080
Db 1246 AGGGTAGAGCTTAAGACCATGGCTTACTGATCAATCCAGTGTACCATGAAGAGATGC 1305
Qy 1081 GAYGYATHTGYMSNMNGCNCNMNG 1109
Db 1306 GATTGTATCTGACACTCAAGACCACTCG 1334

RESULT 8
US-10-039-847A-1
; Sequence 1, Application US/10039847A
; Publication No. US20020183273A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topoluzis, Stavros
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING
; TITLE OF INVENTION: KIDNEY FUNCTION
; FILE REFERENCE: 00-100
; CURRENT APPLICATION NUMBER: US/10/039, 847A
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/244,479
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-10-039-847A-1

Query Match 71.9%; Score 798; DB 13; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

Qy 1 ATGCAAGMNTYNTATHTYNTATYACNTYNTATHTGYGNAAYTGYTGYMSNTGYMGAY 60
Db 226 ATGACCGGCTCATCTTGTCTACCTCTAATCTGCGCAACTTTTGACGCTGCGGAC 285
Qy 61 ACNMSNGCNAACNCCARMSNGCWSNATTAARGCNTYNTMGNAAYCNAAYTMMNGN 120
Db 286 ACTTCTGCAACCCCGAGAGCGCATCCATCAAGCTTGGCCCAACGCCAACCCTCGGCA 345
Qy 121 GAYGABMSNAAYCAYTNTAGAYTNTAYTAYMGNGNGAYGABACNAATHTCARNTAARGN 180
Db 346 GATAGAGCAATCACTCTACAGATCTGTACCGAAGATGAGACATCCAGGTGAAAGGA 405
Qy 181 AAYGANTAYGNTCARMSNCCMMGNTTYCCNAAYMSNTAYCCNMGNAAYTNTYNTYNA 240
Db 406 AAGCGCTACGTCAGAGCTCTAGATTCGGAACAGCTACCCCAAGAACCTGCTCTGCA 465
Qy 241 TGGMNTYNTCAWNSNCARAGAAAYACMGNAATHTCARNTYNTYNTYNTYNTYNTY 300
Db 466 TGGGGCTTCACTCTCAGAGAAATACAGGATACAGCTAGAGTGTGACAAATCAAGTTTGA 525
Qy 301 YTNAGARGAGCNGAAYGAYATHTGYGNTAYGAYTGYTNGARGAGATHTMSN 360

Db 526 TTAGAGAGAGCAAAATGATATCTGATGATGATATTTTGGAAAGTGAAGATATATCC 585
Qy 361 GARACMSNACNAATHTMGNGMNTGTGCGGAGNCAYARGAGTMCNCCMMGNATH 420
Db 586 GAAACCGATCATATTATTAGAGAGAGTGTGAGACCAAGAAATTCCTCCAAAGATA 645
Qy 421 AARMSNMGNAACNAAYCARATHTAATHTAATNTYTAARMSNGAYATYATYTTGNCNAR 480
Db 646 AATCAAGAACGAACCAATTAATCAATTCATAGTCGATGACTACTTGTGCTTAA 705
Qy 481 CCNGNTTAAATHTATYATYAWSNYTYNTGARGAYTTCARCCNGCNGCNGCNGSNGAR 540
Db 706 CCTGATTCAGATTTATATTATCTTGTGAGAAATTTCCAAACCGGAGAGCTTCAAG 765
Qy 541 ACNAAYTGGGARMSNGTACMSWSNATHTSNGNGNTMSNTYAAAYMSNCCMMSNTN 600
Db 766 ACCAAGCTGGGAATGTGTCACAAAGCTTATYTCAGGGGTATCTTAACTCTCATCAGTA 825
Qy 601 ACNAGVCCNAACNTYNTATHTGNGAYGCVNTGNAAYABARATHTGNGARTTYGAYACNGTN 660
Db 826 ACGATCCCACTCTGATTTGGGATGCTCTGAGCAAAAAATTCAGAAATTTGATCACTG 885
Qy 661 GARGAYTNTAARTAYTNTYAAAYCNGARMSNTGGCARGAGAYTNTGARAAYATGTAY 720
Db 886 GAAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAAATCTTGAGAAATGTAT 945
Qy 721 YTNAGAYACNCCMNTAYTMGNGMNSNTYACAYGAYMGNAARMSNAAGTNGAYTNT 780
Db 946 CTGACACCCCTCGGTATCGAGGAGGATACCATGATGACCGAAGTCAAAAGTTGACCTG 1005
Qy 781 GAYGNTYNTAAYGAYGAYGNAARMNTAYVSNTRYACNCCMMGNAAYTAYMSNTYNA 840
Db 1006 GATAGCTCAATGATGATGCCAAGCTTACGTTGCACTCCAGAAATTTACTCGTCAAT 1065
Qy 841 ATTHMGARGARATYNTAATYNTGNAAYATGNTGNTTATYTCNMGNTGYNTYNTGNTCAR 900
Db 1066 ATTAAGAGAGAGCTGAGAGTGGCCAAATGTGCTTCTTCCAGCTGCTCGTGCAG 1125
Qy 901 MGNTRYGNGNGNAAYTGYGNTGYGNAACNGTNAAYTGMGMSNTGYACTGYAAVYSN 960
Db 1126 CGCTGTGAGAGAAATGTGGCTGTGGAACCTGCACTGAGAGTCTGTCACATGCAATTC 1185
Qy 961 GGNABACNGTNAABARTAYCAYGARTYNTGARTYTCARCCNGNCAYATTAARMGN 1020
Db 1186 GGGGAAACCGTGAAGAAATGATCATGAGGTATTAACAGTTGAGCTGGCCATCATCAAGAG 1245
Qy 1021 MNGNGMNGCNAARACATGCGVNTGNTGNAAYATHTCARNTGNAAYCAYGABMGNTGY 1080
Db 1246 AGGGTAGAGCTTAAGACCATGGCTTACTGATCAATCCAGTGTGATCAATCAAGAGATGC 1305
Qy 1081 GAYGYATHTGYMSNMNGCNCNMNG 1109
Db 1306 GATTGTATCTGACACTCAAGACCACTCG 1334

RESULT 9
US-10-226-559-1
; Sequence 1, Application US/10226559
; Publication No. US20030105015A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/10/226, 559
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US/09/540, 224
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/180, 169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9


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SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226) ... (1338)
US-10-226-559-1

Query Match      71.9%; Score 798; DB 15; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAYMGNTAHTTGTCTTAACNTYNAHTHTGCGAAATTTTGTGWSNTGNGAY 60
DB 226 ATGCACGGGCTCATCTTGTCTACACTTAATCTCGGCAACTTTTGGACGCTCGGAC 285
QY 61 ACNMSGNACNCCNCAEWSNCGNMSNATHARGCNTYTMGNAAYGNAAYTMNGMN 120
DB 286 ACTCTGCAACCCCGCAGAGCCATCCATCAAGCTTTGCGACGCCAAGCTCAGGCGA 345
QY 121 GAYGARSNAAYCAVYTNACNGAYTTNTAYMNGNGAYGAPACNATHCARGTNAARGN 180
DB 346 GATGAGACCAATCAGCTCAGAGCTTGACCGAAGAGATGAGACCATCCAGGTGAAGA 405
QY 181 AAYGNTAYGTNCAEWSNCGNMTTTCNAAVMSNTAYCCMNGNAAYTNTYTNACN 240
DB 406 AACGGCTACGTGACAGCTCTGATTCCTGCAAGCTACCCGAGAACCTCTCTGACA 465
QY 241 TGGMNTYTNCAVWSNCAEWSNCAEWSNCAEWSNCAEWSNCAEWSNCAEWSNCA 300
DB 466 TGGCGGCTTCACTCTCAGAGAAATACAGAGATACAGTACAGTGTGACATCACTTGA 525
QY 301 YTNARGARGCNGARAAAGATHTGTGNTAYGAYTTTGTNGARNTGARGAYATHSN 360
DB 526 TTAGAGAGAGAGAAATGATATCTGTAGTATGATTTTGTGAAAGTGAATATATCC 585
QY 361 GABAENMSNACNATHATMNGNCGNMTGTGTGNGCAVYARGNTCCMNGNATH 420
DB 586 GAACACGATACATATTTAGAGAGAGATGTGTGACACAGAGAGATTTCTTCAAGATA 645
QY 421 AARSNMGNACNAAVCARATHAAPATHACNTTVAARWSNGAYATYTTGTNGCNAR 480
DB 646 AAATCAAGAACGAAACCAATTAATCACTTCAAGCTGATGACTTGTGTGCTAAA 705
QY 481 CCNGNTTVAARATHTVTAWSNTYTNARGAYTTTCARCCNGCNGCNGCNGSAR 540
DB 706 CTTGATTCAGATTTATTTATTTCTTGTGAGAGATTTCCAAACCGCAGAGCTTCA 765
QY 541 ACNAAVTOGGARWSNGTNAEWSNMSNATHWSNNGNNTVAAYVMSNCGNMSGN 600
DB 766 ACNAACTGGGAAATCTGCAAGCTTATTTCAAGGATATCTTAACTCTCACTGATA 825
QY 601 ACNAAVTCMNCNTYNAHTGNGAYGNTYTNAYAAARARHTGNGARRTTGYA 660
DB 826 ACAGATCCCACTGATTTGCGAGATCTGTGACAAAAAATTTGCAATTTGATACAG 885
QY 661 GARAYTNTYNTAARTYATYTAACNGARWSNCGARGARVYTNGBAAYATGTAY 720
DB 886 GAATATCTGCTCAAGTACTTCACTCAAGATCATGCGAAGAGATCTTGAATATGAT 945
QY 721 YTNAGVACNCCNMGNTAYMNGNMGNSNTAYCAVYAGNAAARWSNARGNTGAY 780
DB 946 CTGACACCCCTCGATTCAGAGGCAAGTCAATCAATGACCGAAGTCAAAAGTTGAC 1005
QY 781 GAWMAGNTNAYAGVYGCNAAARMTAYMSNTGYACNCGNNAAYTAYMSNMAAY 840
DB 1006 GATAGGCTCAATATATGATGCAAGCTTACAGTTGACCTCCAGGAATTAATCTG 1065
QY 841 ATMGNGARGARYTNAAYTNAGNAAVGTGNTTNTYTTCCNMGNTGYVYNTNGNAR 900
DB 1066 ATTAAGAGAAAGCTGAAGTTGGCAATGTGTCTTCTTCCAGCTTGCTCTCTGAG 1125
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QY 901 MNTGYGNGNNAAYTYGNTGYGNAENGTNAAYTGMNGMNTGYACNTGAAVWSN 960
DB 1126 CGTGTGAGAGAAATTTGGTGTGGAACCTGTCAACTGAGAGCTCTCAGATGAAATTC 1185
QY 961 GGNAAACNNTNAAARATAYCAVAGNTYTNCAFTTGTGARRCCNGNCAVATHAARM 1020
DB 1186 GGGAAACCCGTGAAAAAGTATCAAGAGTATTCAGATTGAGCTCGGCCCATCAAGAG 1245
QY 1021 MNGNMGNGNCAARACNATGAGCNTYTNAGVATHTCARNTGAYCAVYAGMNTGY 1080
DB 1246 AGGGGTAGAGTAAGACATGCTCTGATTTGACATTCAGATTGATCCATGAGATGC 1305
QY 1081 GATGATHTTGYMSNMGNCNCCNMG 1109
DB 1306 GATGATCTGACAGCTCAAGACCACTCG 1334

RESULT 10
US-10-274-638-1
; Sequence 1, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OR INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; FILE REFERENCE: AND METHODS FOR PRODUCING IT
; CURRENT APPLICATION NUMBER: US/10/274,638
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226) ... (1338)
US-10-274-638-1

Query Match      71.9%; Score 798; DB 15; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAYMGNTAHTTGTCTTAACNTYNAHTHTGCGAAATTTTGTGWSNTGNGAY 60
DB 226 ATGCACGGGCTCATCTTGTCTACACTTAATCTCGGCAACTTTTGGACGCTCGGAC 285
QY 61 ACNMSGNACNCCNCAEWSNCGNMSNATHARGCNTYTMGNAAYGNAAYTMNGMN 120
DB 286 ACTCTGCAACCCCGCAGAGCCATCCATCAAGCTTTGCGACGCCAAGCTCAGGCGA 345
QY 121 GAYGARSNAAYCAVYTNACNGAYTTNTAYMNGNGAYGAPACNATHCARGTNAARGN 180
DB 346 GATGAGACCAATCAGCTCAGAGCTTGACCGAAGAGATGAGACCATCCAGGTGAAGA 405
QY 181 AAYGNTAYGTNCAEWSNCGNMTTTCNAAVMSNTAYCCMNGNAAYTNTYTNACN 240
DB 406 AACGGCTACGTGACAGCTCTGATTCCTGCAAGCTACCCGAGAACCTCTCTGACA 465
QY 241 TGGMNTYTNCAVWSNCAEWSNCAEWSNCAEWSNCAEWSNCAEWSNCAEWSNCA 300
DB 466 TGGCGGCTTCACTCTCAGAGAAATACAGAGATACAGTACAGTGTGACATCACTTGA 525
QY 301 YTNARGARGCNGARAAAGATHTGTGNTAYGAYTTTGTNGARNTGARGAYATHSN 360
DB 526 TTAGAGAGAGAGAAATGATATCTGTAGTATGATTTTGTGAAAGTGAATATATCC 585
QY 361 GABAENMSNACNATHATMNGNCGNMTGTGTGNGCAVYARGNTCCMNGNATH 420
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Db 586 GAAACACGATCAATTATTAGAGAGATGCTGAGACCAAGAACTCTCCAAGATA 645
Qy 421 AARMSNGMNCNAAYCARATHAATACNTTYAARMSNGAYATYATYGTNGCNAR 480
Db 646 AATCAAGAAAGCAACCAATTAATCACTTCAAGTCGAGTCACTTGTGTGCTTAA 705
Qy 481 CCNGNTTYAARATHATYATYATYATYATYATYATYATYATYATYATYATYATY 540
Db 706 CCGTGATTCAGATTTATATATCTTCTGCTGAGAAATTTCCACCCGACGCTTCAGAG 765
Qy 541 ACNAAYTGGAGARMSNGTNAACMSWSNATHSNGNGTNSNTAYAAVMSNCMSNGTN 600
Db 766 ACCAAGCTGGAATCTGTCAACAGCTATTTCAAGGGATCTCTAATCTCCATCAGTA 825
Qy 601 ACNAGYCCNACNTYATYATYATYATYATYATYATYATYATYATYATYATYATY 660
Db 826 ACAGATCCCACTGTGATGCGAGTCTGTGACAAAATAATYAGAAATYATGATACGTG 885
Qy 661 GARGAYTNTYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 720
Db 886 GAGATCTGCTCAAGTACTTCAATCCAGAGTCAATGCGAAGATCTTGAGAAATATGTAT 945
Qy 721 YTNAGYACNCCNMNTAYTMNGMNGMNSNTAYCAYAGYMGNAARMSNARGTNGAYTN 780
Db 946 CTGGAACACCCCTCGGTATCGAGGAGGTCAATACCATGACCGAAGTCAAAAGTTGACCTG 1005
Qy 781 GAYMNTYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 840
Db 1006 GATAGGCTCAATYATYATYATYATYATYATYATYATYATYATYATYATYATY 1065
Qy 841 ATTHMGNGARBYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 900
Db 1066 ATAAGAGAAAGCTGAAAGTGTGCGCAATGTGTCTTTTCCACCTGCTCTGCTGAG 1125
Qy 901 MENTGYGNGMNAAYTYGNTGYGNAACNGTNAAYTGAMGMSNTGYACNTGYAAYWSN 960
Db 1126 CGCTGTGAGGAATYTGCTGTGGAACCTGTCACTGAGAGTCTGTGCAATGCAATCA 1185
Qy 961 GGNABACNGTNAARATYATYATYATYATYATYATYATYATYATYATYATYATY 1020
Db 1186 GGGGAAACCGTGAAGAAATGATCATGAGTATTAACAGTTGAGCTGCGCACATCAAGAG 1245
Qy 1021 MNGMNGMNGMNAARATYATYATYATYATYATYATYATYATYATYATYATYATY 1080
Db 1246 AGGGGTAGAGTAAAGACCATGCTCTAGTTACATCCAGTTGATCCACATGAACGATGC 1305
Qy 1081 GAYTGYATHTGYMSMNSMNGCNCNMNG 1109
Db 1306 GATTGTATCTGACGCTCAAGACCACTCG 1334

RESULT 11
US-10-365-095-1
; Sequence 1, Application US/10365095
; Publication No. US20030224488A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Moore, Margaret D.
; APPLICANT: Swiderex, Kristine M.
; APPLICANT: Birk, Carl W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
; FILE REFERENCE: 01-33
; CURRENT APPLICATION NUMBER: US/10/365,095
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 60/355,882
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (226)...(1338)
; US-10-365-095-1

Query Match 71.9%; Score 798; DB 15; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2,98-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

Qy 1 ATGCAVGNATYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 60
Db 226 ATGACCGGCTCACTTGTCTTACACTATYATYATYATYATYATYATYATYATYATY 285
Qy 61 ACMSNGMNCNCCNARMSNGMNSNATHARCNTYATYATYATYATYATYATYATYATY 120
Db 286 ACTTCTGCAACCCCGCAGAGGATCTCATCAACCTTGTGCCAAGCCCACTCAGGGA 345
Qy 121 GAYGARSNAAYCAAYTNACGAYATYATYATYATYATYATYATYATYATYATYATY 180
Db 346 GATGAGACATCACTCAAGACTGTGACCGAAGAGATGAGACATCCAGGTGAAAGGA 405
Qy 181 AAYGNTATYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 240
Db 406 AAGGCTACGTCAGAGATCTTGAATCCCAAGCTCAAGCTCAAGCTCAAGCTCA 465
Qy 241 TGGMNTYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 300
Db 466 TGGGCTTCACTCTCAGAGAAATCAAGATCAAGTACAGTATGATGATGATGATGAT 525
Qy 301 YTNAGARCGNGARAAVGAATHTGYMNTAYATYATYATYATYATYATYATYATYATY 360
Db 526 TTAAGAGAAAGCAAAATGATATCTGATGATATYATYATYATYATYATYATYATYATY 585
Qy 361 GABACMSNACNATHATTHMGNGMNTGTGYGNGCAVYARAGRTNCCNMNGNATH 420
Db 586 GAAACCAAGTACATYATYATYATYATYATYATYATYATYATYATYATYATYATY 645
Qy 421 AARMSNGMNCNAAYCARATHAATACNTTYAARMSNGAYATYATYATYATYATYATY 480
Db 646 AATCAAGAAAGCAACCAATTAATCACTTCAAGTCGAGTCACTTGTGTGCTTAA 705
Qy 481 CCNGNTTYAARATHATYATYATYATYATYATYATYATYATYATYATYATYATY 540
Db 706 CCGTGATTCAGATTTATATATCTTCTGCTGAGAAATTTCCACCCGACGCTTCAGAG 765
Qy 541 ACNAAYTGGAGARMSNGTNAACMSWSNATHSNGNGTNSNTAYAAVMSNCMSNGTN 600
Db 766 ACCAAGCTGGAATCTGTCAACAGCTCTAATYATYATYATYATYATYATYATYATY 825
Qy 601 ACNAGYCCNACNTYATYATYATYATYATYATYATYATYATYATYATYATYATY 660
Db 826 ACAGATCCCACTGTGATGCGAGTCTGTGACAAAATAATYAGAAATYATGATACGTG 885
Qy 721 YTNAGYACNCCNMNTAYTMNGMNGMNSNTAYCAYAGYMGNAARMSNARGTNGAYTN 780
Db 946 CTGGAACACCCCTCGGTATCGAGGAGGTCAATACCATGACCGAAGTCAAAAGTTGACCTG 1005
Qy 781 GAYMNTYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 840
Db 1006 GATAGGCTCAATYATYATYATYATYATYATYATYATYATYATYATYATYATY 1065
Qy 841 ATTHMGNGARBYATYATYATYATYATYATYATYATYATYATYATYATYATYATY 900
Db 1066 ATAAGAGAAAGCTGAAAGTGTGCGCAATGTGTCTTTTCCACCTGCTCTGCTGAG 1125
Qy 901 MENTGYGNGMNAAYTYGNTGYGNAACNGTNAAYTGAMGMSNTGYACNTGYAAYWSN 960
Db 1126 CGCTGTGAGGAATYTGCTGTGGAACCTGTCACTGAGAGTCTGTGCAATGCAATCA 1185
Qy 961 GGNABACNGTNAARATYATYATYATYATYATYATYATYATYATYATYATYATY 1020

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Db      1186 GGGAAAACCGTGAAGATATCATGAGTATTACAGTTTGAGCCCTGGCCACATCAAGAG 1245
      1021 MNGGMMNGCNAARAACNAATGGCNTYNTGNGAYATHCAATYTGAYCAYCAARMNGTGY 1080
      1246 AGGGGTAGAGCTAAGACCATGTGCTAGTTCATCCAGTTCGATCACCATGAACGATGC 1305
Qy      1081 GAYTGAATHTGYSMNSMNGCNCNMNG 1109
      1306 GATTGTATCTGCAGCTCAAGACCCTCG 1334

RESULT 12
US-10-606-055-1
; Sequence 1, Application US/10606055
; Publication No. US20040043027A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Topouzis, Stavros
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
; FILE REFERENCE: 00-79
; CURRENT APPLICATION NUMBER: US/10/606,055
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US/09/808,972
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/235,295
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/132,250
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
US-10-606-055-1

Query Match      71.9%; Score 798; DB 16; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
Qy      1 ATGCAYMGNATNATHTTGTATAYACNVTNATHTGCGNAAYTTTGYMSNTGTMNGAY 60
      226 ATGACCGGCTCATCTTGTGTACATCTATCTGCGCAACTTTTGACGCTGTGCGGAC 285
Db      61 ACNMSNGCNAACCCGAGAGGAGCATCATCAAGCTTTGCGCAACGCGCAACTCAAGCGA 345
      286 ACTTCTCAACCCGAGAGGAGCATCATCAAGCTTTGCGCAACGCGCAACTCAAGCGA 345
Qy      121 GAYGARSNAAYCAAYTNACGAYTNTAYVGNMNGNAYGABACNAHCAHCAHCAHCAHCAH 180
      346 GATAGAGCAATCACTTACGACTTGTACCGAAGATAGACATCCAGGGAAGGA 405
Db      181 AAYGANTAYGTCNARMSNCCNMNTTTCNAAAYMSNTAYCCNMNAAAYTNTNTNACN 240
      406 AACGGCTACGTGAGAGTCCAGATTCGCCAAGCCTACCCGAGAACCTGCTCTGACA 465
Qy      241 TGGMGNATNCAVMNCAAGAAAYACMGNAATTCARTTNGTNTTGAAYAAVCARTTYGAN 300
      466 TGGCGGCTTACTTCTGAGGAATACAGGATACAGTACTGTTGCAATCAGTTTGA 525
Db      301 YTMGARBARCNGARAAYGAYATHTGYMNTAYGAYTTTGTNABGTNABGAYATHMNS 360

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Db      526 TTAAGAGAGCAGAAATGATATCTAGATATGATTTTGGAAAGTTGAAGATATATCC 585
      361 GARACMSNAACNATHATMNGMNGMNTGGTGYGNCAYARAGARNTCCNMGNATH 420
      586 GAACCAAGTACCATTAATTAGAGAGCATGGTGTGACACAAAGAAAGTTCTCCCAAGATA 645
Qy      421 AARSNMGNACNAAYCARATHAARATHACNTTYAARNSNGAYATYATTTGTNGCAAR 480
      646 AATCAAGAAACGAACCAATTAATAATCAATTCAGTCCATGACTCTTGTGGCTAAA 705
Db      481 CCNGNTTAAARATHATYATVMSNTYNTNGAGAYTTTGCARCCNGCNGCNGCNGSGAR 540
      706 CTGTGATTCAGATTTATTTATCTTCTGAGAAATTTCCAAACCGAGAGCTTCAAG 765
Qy      541 ACNAAATGGAGARMSNGTACNMSNMTATMSNGNGTMSNTAYAAVMSNCCNMSNGTN 600
      766 ACCAACTGGGAATCTGCAACAAGCTCTATTCAAGGGTATCCTATACTCCTCAATCAGTA 825
Db      601 ACNAYCCNACNATNATHGNGAYGCTNTGAYAAABAATHGNCARTTYGAYACNGTN 660
      826 ACCGATCCACTCTGATTTGGATGCTGAGACAAAAAATTCAGAAATTTGATACAGTG 885
Qy      661 GARGAYTNTNAAATTAATTAAYTAAVCCNGARMSNTGCGARAGAYTTNGARAATGTAY 720
      886 GAAGATCTGCTCAAGTACTTCAATCCAGAGTCAATGCGCAAGAAATCTTGAAATATGTAT 945
Qy      721 YTMGAYACNCCNMNGTAYMNGMNGMNSNTAYCAVAYGNAARMSNAARNTNGAYTN 780
      946 CTGACACCCCTCGGTATCGAGGACAGTCAATCAATGACCGAATTCAGAAAGTTGACCTG 1005
Qy      781 GAYMGNATNAAAYGAYGNGCNAARMNTAYMSNTGYACNCCNMNAAAYTAYMSNGTMAAY 840
      1006 GATAGCTCAATATATATGCTCAAGCTTACAGTTGACATCCAGAAATTAATCTGCTCAAT 1065
Db      841 ATMNGARBARNTNAAATYNTGCAAYGNTTNTTTCNMNGTGYTNTNGTNCAR 900
      1066 ATAGAGAGAGAGCTGAAGTTGGCCAAATGTGCTCTTTCACAGTTGCTCCTCGTGCAG 1125
Qy      901 MNTGYGNGNAAAYGNGANTGYGNAACNTNAAATGGMKMSNTGYACNTGYAAYMSN 960
      1126 CGCTGTGAGAGAAATGTGTGCTGTGAACTGTCACTGAGAGGCTCGCAATGCAATTTCA 1185
Db      961 GGNABACNTNAAARATTAAYCAVAGARNTYNTCAATTTGAGCCNGCNGCAVATTAARMGN 1020
      1186 GGGAAAACCGTGAAGATATCATGAGTATTACAGTTTGAGCTTGGCCACATCAAGAG 1245
Qy      1021 MNGGMMNGCNAARAACNAATGGCNTYNTGNGAYATHCAATYTGAYCAYCAARMNGTGY 1080
      1246 AGGGGTAGAGCTAAGACCATGTGCTAGTTCATCCAGTTCGATCACCATGAACGATGC 1305
Db      1081 GAYTGAATHTGYSMNSMNGCNCNMNG 1109
      1306 GATTGTATCTGCAGCTCAAGACCCTCG 1334

RESULT 13
US-10-086-623-7
; Sequence 7, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTTERL, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THE
; FILE REFERENCE: 1064/4833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04

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PRIORITY APPLICATION NUMBER: US 60/107,852
PRIORITY FILING DATE: 1998-11-10
PRIORITY APPLICATION NUMBER: US 60/113,997
PRIORITY FILING DATE: 1998-12-28
PRIORITY APPLICATION NUMBER: US 60/150,604
PRIORITY FILING DATE: 1999-08-26
PRIORITY APPLICATION NUMBER: US 60/157,108
PRIORITY FILING DATE: 1999-10-04
PRIORITY APPLICATION NUMBER: US 60/157,756
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: US 09/438,046
PRIORITY FILING DATE: 1999-11-10
PRIORITY APPLICATION NUMBER: US 09/691,200
PRIORITY FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 2253
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (176)..(1288)
OTHER INFORMATION:
US-10-086-623-7

Query Match      71.9%; Score 798; DB 13; Length 2253;
Best Local Similarity 56.4%; Pred. No. 3.4e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAAGNNTNATTTTGTATTAACNTTATHTGTCGNAAYTTTGYGWSNTGYMGNAY 60
DB 176 ATGCAAGNNTNATTTTGTATTAACNTTATHTGTCGNAAYTTTGYGWSNTGYMGNAY 235
QY 61 ACNWSNGNACNCCNCAWSNGNWSNATTHARGCNNTNMGNAAYGCAAYTNMGNNGN 120
DB 236 ACTTCTGCAACCCGCAAGGCAATCCATCAAGCTTTGCCGAGCCCACTGCTGCGGAC 295
QY 121 GAYGARSNAAYCAVYTTNACNGAYTTTATYMGNGNGAYGACNATHTCAGTNAARBN 180
DB 296 GATGAGAGCAATCACTCTCAAGACTTGTACCGAAGATGAGACATCCAGGTGAAGA 355
QY 181 AAYGANTYATGTCNARWSNCCNMGNTTCCNAAVYNTYCCNMGNAAYTYTNTYNTACN 240
DB 356 AACGCTACGTCGACAGTCTAGATTCCCGAACAGCTCCCAAGAACCTGCTCTGACA 415
QY 241 TGGMGNNTNCAVWSNCAAGABAAYACNMGNAHTCARNTNGTNTTYGAYAAVCAPTTYG 300
DB 416 TGGGGGCTTCACTCTCAAGAGATACAGGATACAGTATGTTTGACAACTCACTTGA 475
QY 301 YTNAGARGCNGARBAAYGAYATHTGVTGNTAYGAYTTTGTNGARGTNGARGAYTTHSN 360
DB 476 TTAAGGAAAGCAAAATGATATCTGTAGTATGATTTTGTGGAAGTTGGAAGATATATCC 535
QY 361 GARCNWSNACNATHTATMGNGNMGNTGTGNGNCAVYARAGTNCNCCNMGNAHT 420
DB 536 GAACACGCTACATTAATTAAGAGAGATGAGTGTGACCAAGAGTCTCTCAAGATA 595
QY 421 AARSMNMGNAAYCARATHAARATHACNTTYAARMSNGAYGATTAATYVGTNGCNAR 480
DB 596 AATCAAGAGCAAGCAATTAATTAATCACTCAAGTCCAGTACCTTGTGCTAA 655
QY 481 CCNGNTTAAATHTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 656 CCTGATTCAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 715
QY 541 ACNAAATGCGARMSNCTNACNWSNMTNTHSNGNNGTNGTNTAAVWSNCCNMGNTN 600
DB 716 ACCAATGCGAATCTGTCAACAGCTCTAATTTCAAGGAGTATCTTAACTCTTCACTCA 775
QY 601 ACNGAYCCNACNNTYATHTGNGAYGNCNTNGAYAAARAATHTGNGARTTYGAYACNGTN 660
DB 776 ACGGATCCCACTCTGATTTGCGGATGCTCTGACAAATAATTTGCAAGATTTGATCAGTG 835
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QY 661 GARGAYTNTNARTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720
DB 836 GAAGATCTGCTCAAGTACTTCAATCCAGACGATCGCAAGAGATCTTGAGAAATATGAT 895
QY 721 YTNAGAYACNCCNMGNTAYMGNGNMGWSNNTAYCAVAYMGNAARWSNARGTNGAYTN 780
DB 896 CTGACACACCTCGGTATTCAGAGGACAGGTCAATACATGACCGGAAGTCAAAAGTGA 955
QY 781 GAYMGNNTNAAVYAGVAGCAAAAMGNNTAYMSNTGYACNCCNMGNAATTAATWSNNTAY 840
DB 956 GATAGGCTCAATGATGATGACCAAGCTTACAGTTCACCTCCAGAAATTAATCTCGTCAAT 1015
QY 841 ATTHMNGARGARYNNAAYTNGNCAAYGTNGNTNTTYTCCNMGNTGYTYTNGTNCAR 900
DB 1016 ATPAAGAGAGAGCTGAACTGGAATGTCCTTCTTTTCAAGCTTCTGCTGAG 1075
QY 901 MANTGYGNGNNAAYTGYGNTGYGNAACNGTNAAYTGAMWSNNTGYACNTGYAAVWSN 960
DB 1076 CGCTGTGAGGAAATTTGTGGCTGTGGAACCTGCACTGAGAGTCTGCAATGCAATTC 1135
QY 961 GGNARACNCTNAAARTATYCAVARGTNTNCARTTYGARCCNGNCAVATHAARBN 1020
DB 1136 GGGAAACCGTGAATAAGTATCATGAGGTATTAACAGTTCAGCTGACATCAAGAG 1195
QY 1021 MNGNMGNGNNAARACNATGTCNNTNGTNGAYATHTCARNTNGAYCAVAGARGMNTGY 1080
DB 1196 AGGGGTAGAGCTTAAGACCATGCTCTTACTTATGATCATCCAGTTCACATGAGAGATGC 1255
QY 1081 GAYTGYATHTGYWSNWSNMGNCNCCNMG 1109
DB 1256 GATTGTATCTGACGCTCAAGACCACTCG 1284

RESULT 14
US-10-260-539-7
Sequence 7, Application US/10260539
Publication No. US20030073637A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LI, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: TUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HEIDIN, Carl-Henrik
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF
FILE REFERENCE: 1064/448332
CURRENT APPLICATION NUMBER: US/10/260,539
PRIORITY FILING DATE: 2002-10-01
PRIORITY APPLICATION NUMBER: US/10/086,623
PRIORITY FILING DATE: 2000-03-04
PRIORITY APPLICATION NUMBER: US 60/107,852
PRIORITY FILING DATE: 1998-11-10
PRIORITY APPLICATION NUMBER: US 60/113,997
PRIORITY FILING DATE: 1998-12-28
PRIORITY APPLICATION NUMBER: US 60/150,604
PRIORITY FILING DATE: 1999-08-26
PRIORITY APPLICATION NUMBER: US 60/157,108
PRIORITY FILING DATE: 1999-10-04
PRIORITY APPLICATION NUMBER: US 60/157,756
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: US 09/438,046
PRIORITY FILING DATE: 1999-11-10
PRIORITY APPLICATION NUMBER: US 09/691,200
PRIORITY FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 2253
TYPE: DNA
ORGANISM: Homo sapiens
```

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176) ..(1288)
; OTHER INFORMATION:
US-10-260-539-7

```

```

Query Match      71.9%; Score 798; DB 14; Length 2253;
Best Local Similarity 56.4%; Pred. No. 3.4e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

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QY 1 ATGCATMGNTYNAHTTGTGTNTAATACNTYNAHTHTGTCGNAAYTTGTGYSNTGNGNGAY 60
DB ATGCACCGGCTCATCTTGTCTACACTCTAATCTGGCGAACTTTTGACGCTGTGGGAGC 235
QY 61 ACNWSNGNACNCCNCRKSNCGNMSNATHARGCNTYTMGNAAAGCNAAAYTTMGMNGN 120
DB ACTTCGCAACCCCGCAGAGCGCATCTCAAAAGCTTTGGCAGCCCACTCGAGGGA 295
QY 121 GAYGARWSNAAYCAAYTNAACGAYTNTAYMGMNGAGAYGARACNAHTCARGTNAARGN 180
DB GATGAGAGCAATCACTCAAGACTGTACCGAAGAGATGACCAATCCAGGTGAAGA 355
QY 181 AAYGNTAYGTNCARWSNCCNMGNTTCCNAAYSNTAYCCMNGNAAYTNTYTNACN 240
DB AACGGCTACGTCAAGATCTTAGATTTCCGGAACAGTACCAGGAACTGCTCTGACA 415
QY 241 TGGMGNTYNAWSNCRGABAAAYACNMGNAHTCARNTNGTNTTGAAYACARTTYGN 300
DB TGGCGGCTTCACTCTCAGAGAAATACAGATACAGCTTAGTGTGACATCAATGTTGA 475
QY 301 YTNGARARGCNGARAAAYATHTGYMNTAYGAYTTGTNGARGTNGARGAYATHTWSN 360
DB TTAGAGGAAGCAGAAATGATCTGTAGATGATTTTGGGAAGTTGAAGATATATCC 535
QY 361 GABACMSNACNAHTATHMNGNNGNTGTGTGNCAYARARGTNCNCCMNGNATH 420
DB GAACACAGTACCATTAATTAGAGGAGATGTGTGACCAAGAGATTCCTCCAAAGATA 595
QY 421 AARSMNMGNAACNACARATHAARATHACNTTAYARMSNGAYATYATTTGTNGCNAR 480
DB AAATCAAGAACGACCAATTAATTAATCACTTCAAGTCCAGTACTTGTGTCTDAA 655
QY 596 AATCAAGAACGACCAATTAATTAATCACTTCAAGTCCAGTACTTGTGTCTDAA 655
DB CCTGATTCAGAGATTAATTAATTTCTTGTGGAAGATTTCCAACCGCAGGCTTCAAG 715
QY 541 ACNAAVTGGARWSNGTNAACNWSNNAHTHNSNGNCGNMSNTAYAAYSNCCNWSN 600
DB ACNAACTGGAAATCTGTACAAAGCTCTAATTCAGGGGTATCTTAATCTTCCATCAGTA 775
QY 601 ACNGAATCCNACNTYNAHTGNCAGAYCNYTNGAYARARATHGNCARTTTGAACNGTN 660
DB ACGGATCCCACTGTGATTTGGGAGTGTCTGGAACAAAAATTTGAGAAITTTGATACGTG 835
QY 776 ACGGATCCCACTGTGATTTGGGAGTGTCTGGAACAAAAATTTGAGAAITTTGATACGTG 835
DB GABAYTNTYNTNARATYTTTAAATCCNGARWSNTGGCARGARAYTNGARAAATGTAY 720
QY 661 GABAYTNTYNTNARATYTTTAAATCCNGARWSNTGGCARGARAYTNGARAAATGTAY 720
DB GAAATCTGTCTCAAGTACTTCAATCCAGAGTCATGTGGAAGAAATCTTGAATAATATAT 895
QY 836 GAAATCTGTCTCAAGTACTTCAATCCAGAGTCATGTGGAAGAAATCTTGAATAATATAT 895
DB YTNAAVACNCCNMGNTYTMGMNGNMSNTAYCAYAYMGNARMSNARNTNGAYTN 780
QY 721 YTNAAVACNCCNMGNTYTMGMNGNMSNTAYCAYAYMGNARMSNARNTNGAYTN 780
DB CTGACACCCCTCGGTATCCAGGAGGTCTATACATGACCGAAGGTCAAAAGTTGACCTG 955
QY 896 CTGACACCCCTCGGTATCCAGGAGGTCTATACATGACCGAAGGTCAAAAGTTGACCTG 955
DB GATAGGCTCAATGATGATGCGCAAGCTTACGTTGACCTCCAGGATTTCTCGGTCAAT 1015
QY 781 GAYMGNATNAAYGAYGACNAAAMGNTAYWSNTGYACNCCMNGNAAYTAYWSNATAY 840
DB GATAGGCTCAATGATGATGCGCAAGCTTACGTTGACCTCCAGGATTTCTCGGTCAAT 1015
QY 841 ATTHMGNARGARYNTNARATYTMGNAAAYTNGTNTTTCNMGNTGYTNTYNTNGCAR 900
DB ATTHMGNARGARYNTNARATYTMGNAAAYTNGTNTTTCNMGNTGYTNTYNTNGCAR 900
QY 1016 ATTAAGAGAAAGCTGAAGTGTGGCAATGTGTCTTCTTCCACGTTGCTCTGTCAG 1075
DB ATTAAGAGAAAGCTGAAGTGTGGCAATGTGTCTTCTTCCACGTTGCTCTGTCAG 1075
QY 901 MGNATYNGNNGNAAVTGTGNTGTGNGACNCTNAAYYTGNGMSNTGYACNTGYAAYSN 960
DB MGNATYNGNNGNAAVTGTGNTGTGNGACNCTNAAYYTGNGMSNTGYACNTGYAAYSN 960
QY 1076 CGCTGTGGAGAAATTTGTGCTGTGAACTGTCACTGGAAGTCTGCAATCAATCAATTA 1135
DB CGCTGTGGAGAAATTTGTGCTGTGAACTGTCACTGGAAGTCTGCAATCAATCAATTA 1135

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QY 961 GGNAAACNCTNAARATAYCAVARGNTYNTGARTTYGARCCNGNCAYATHAARMGN 1020
DB GGGAAAAACCGTGAAGAAATATCATGAGGTATTAACGTTTGAAGCTGGCCATCATCAAGTC 1195
QY 1021 MNGNMGNCGNARACNATGCGNTYNTGNTNAYATHTCARNTNGAYCAVARGMNTGY 1080
DB AGGGGTAGAGTAAAGACCATGCTCTAGTTGACATCCAGTTGATCAATCAATGAACGATGC 1255
QY 1081 GATGYATHTGYMSNMGNCNCCNMG 1109
DB GATGTATCTGACACTCAAGACCACTG 1284

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RESULT 15
US-10-246-091-4
; Sequence 4, Application US/10246091
; Publication No. US20030203844A1
; GENERAL INFORMATION:
; APPLICANT: Delfant, Kloumarr
; APPLICANT: Janson, Ann Marie
; APPLICANT: Kuhn, Georg
; APPLICANT: Plate, Karlheinz
; APPLICANT: Schnazer, Anne
; APPLICANT: Wachs, Frank-Peter
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: Treatment of Central Nervous System Disorders
; FILE REFERENCE: 21882-504 (PDGF/VEGF)
; CURRENT APPLICATION NUMBER: US/10/246,091
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,381
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/326,044
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-246-091-4

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Query Match      71.9%; Score 798; DB 15; Length 2253;
Best Local Similarity 56.4%; Pred. No. 3.4e-202;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
QY 1 ATGCATMGNTYNAHTTGTGTNTAATACNTYNAHTHTGTCGNAAYTTGTGYSNTGNGNGAY 60
DB ATGCACCGGCTCATCTTGTCTACACTCTAATCTGGCGAACTTTTGACGCTGTGGGAGC 235
QY 61 ACNWSNGNACNCCNCRKSNCGNMSNATHARGCNTYTMGNAAAGCNAAAYTTMGMNGN 120
DB ACTTCGCAACCCCGCAGAGCGCATCTCAAAAGCTTTGGCAGCCCACTCGAGGGA 295
QY 121 GAYGARWSNAAYCAAYTNAACGAYTNTAYMGMNGAGAYGARACNAHTCARGTNAARGN 180
DB GATGAGAGCAATCACTCAAGACTGTACCGAAGAGATGACCAATCCAGGTGAAGA 355
QY 181 AAYGNTAYGTNCARWSNCCNMGNTTCCNAAYSNTAYCCMNGNAAYTNTYTNACN 240
DB AACGGCTACGTCAAGATCTTAGATTTCCGGAACAGTACCAGGAACTGCTCTGACA 415
QY 241 TGGMGNTYNAWSNCRGABAAAYACNMGNAHTCARNTNGTNTTGAAYACARTTYGN 300
DB TGGCGGCTTCACTCTCAGAGAAATACAGATACAGCTTAGTGTGACATCAATGTTTGA 475
QY 301 YTNGARARGCNGARAAAYATHTGYMNTAYGAYTTGTNGARGTNGARGAYATHTWSN 360
DB TTAGAGGAAGCAGAAATGATCTGTAGATGATTTTGGGAAGTTGAAGATATATCC 535
QY 361 GABACMSNACNAHTATHMNGNNGNTGTGTGNCAYARARGTNCNCCMNGNATH 420
DB GAACACAGTACCATTAATTAGAGGAGATGTGTGACCAAGAGATTCCTCCAAAGATA 595

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:58:20 ; Search time -1869.59 Seconds
(without alignment)
-3116.645 Million cell updates/sec

Title: US-09-876-813-6
Perfect score: 1110
Sequence: 1 atcgacmgynhcnathtygtc.....gywnawmngnccnccmngn 1110

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: geneeqn1980s:*
- 2: geneeqn1990s:*
- 3: geneeqn2000s:*
- 4: geneeqn2001s:*
- 5: geneeqn2001bs:*
- 6: geneeqn2002as:*
- 7: geneeqn2002bs:*
- 8: geneeqn2003as:*
- 9: geneeqn2003bs:*
- 10: geneeqn2003cs:*
- 11: geneeqn2003ds:*
- 12: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798	71.9	1110	3 AAC81556	AAC81556 Human gro
2	798	71.9	1110	4 AAF24197	AAF24197 Human veg
3	798	71.9	1110	10 ACA64110	ACA64110 Degenerate
4	798	71.9	1110	12 ADJ32759	ADJ32759 Human zve
5	798	71.9	1728	4 AAS04498	AAS04498 Human pdg
6	798	71.9	1828	4 AAS04492	AAS04492 Human fct
7	798	71.9	1828	6 ABN84524	ABN84524 Human fct
8	798	71.9	1828	6 ABS63515	ABS63515 Human fct
9	798	71.9	1828	10 ADK18626	ADK18626 Human pdg
10	798	71.9	1882	3 AAA51541	AAA51541 SEQ. ID.
11	798	71.9	1882	3 AAC81555	AAC81555 Human gro
12	798	71.9	1882	4 AAH47772	AAH47772 Human zve
13	798	71.9	1882	6 ABS68643	ABS68643 Human cdn
14	798	71.9	1882	6 ABN84420	ABN84420 Human zve
15	798	71.9	1882	8 ABG73239	ABG73239 Human zve
16	798	71.9	1882	8 ABY93177	ABY93177 DNA encod
17	798	71.9	1882	8 ACC47941	ACC47941 Human pdg
18	798	71.9	1882	9 AAD58378	AAD58378 Human pla
19	798	71.9	1882	10 AAD64615	AAD64615 Human zve
20	798	71.9	1882	10 ADG47745	ADG47745 Human zve
21	798	71.9	1882	10 ACA64109	ACA64109 Human cdn

22	798	71.9	1882	12 ADJ32754	ADJ32754 Human zve
23	798	71.9	1882	12 ADL67181	ADL67181 Human zve
24	798	71.9	2253	3 AAD00738	AAD00738 Human pla
25	798	71.9	2253	6 AB080246	AB080246 PDGF-D CD
26	798	71.9	3736	6 AAD25488	AAD25488 Human lpb
27	798	71.9	3739	10 ADG65192	ADG65192 Cell prol
28	798	71.9	3798	5 AAH46939	AAH46939 Human sec
29	798	71.9	3798	5 AAS58475	AAS58475 Human sec
30	798	71.9	3808	12 ADO20112	ADO20112 Human veg
31	798	71.9	3853	4 AAF24196	AAF24196 Human veg
32	798	71.9	4153	12 ADQ23870	ADQ23870 Human sof
33	798	71.9	4153	12 ADQ22990	ADQ22990 Human sof
34	798	71.9	4153	12 ADQ24013	ADQ24013 Human sof
35	797.6	71.9	4001	5 AAH46957	AAH46957 Human sec
36	797.6	71.9	4001	6 ABS58493	ABS58493 Human sec
37	796.4	71.7	1828	12 ADM57642	ADM57642 Human fct
38	757.4	68.2	1162	4 AAS21336	AAS21336 Human cdn
39	757.4	68.2	1162	6 ABL88828	ABL88828 Human pro
40	757.4	68.2	1162	6 ABL95717	ABL95717 Human ang
41	757.4	68.2	1162	8 ACA03695	ACA03695 CDNA enc
42	757.4	68.2	1162	8 ABX89233	ABX89233 DNA encod
43	757.4	68.2	1162	8 ACD41887	ACD41887 Human sec
44	757.4	68.2	1162	8 ACA04116	ACA04116 Human cdn
45	757.4	68.2	1162	9 ADA45704	ADA45704 Novel hum

ALIGNMENTS

RESULT 1
AAC81556
ID AAC81556 strand; DNA; 1110 BP.
AC AAC81556;
DT 09-MAR-2001 (first entry)
DE Human growth factor homologue zveg4, degenerate DNA, SEQ ID NO:6.
XX Human; zveg4; growth factor homologue; VEGF/PDGF family; CUB domain;
XX PDGF-like activity; mitogenic; osteogenic; neovascularisation;
XX tissue repair; proliferation; differentiation; liver damage;
XX neurodegenerative; Alzheimer's disease; multiple sclerosis;
XX peridental disease; bone fracture; wound healing; vulnerability; ischaemia;
XX immunomodulation; hepatic; ds.
XX Homo sapiens.
OS Synthetic.
OS
XX
XX
XX PN WO200066736-A1.
PD 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US040047.
XX
XX 03-MAY-1999; 99US-00304216.
XX 10-NOV-1999; 99US-0164463P.
XX 04-FEB-2000; 2000US-0180169P.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI WPI; 2000-687541/67.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
XX e.g. for treating liver damage, ischemia, multiple sclerosis and
XX Alzheimer's disease.
XX
XX Claim 34; Page 114; 143pp; English.
XX
XX The invention relates to the human growth factor homologue zveg4
XX (AAB48553), and nucleic acids encoding it (AAC81555). Zveg4 is a member
XX CC

CC are used as modulating agents or as targets for developing modulating
CC agents to regulate a variety of cellular processes e.g. cell
CC proliferation, differentiation, migration and wound repair. VEGF-G
CC modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid
CC are used to treat a subject with aberrant VEGF-G protein or nucleic acid
CC expression or activity e.g. deregulated cell growth, such as cancer,
CC hyperproliferic bone disorders, disorders involving aberrant angiogenesis
CC e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid
CC arthritis. VEGF-G gene expression is inhibited through the administration
CC of antisense molecules or ribozymes and by targeting the regulatory
CC region of VEGF-G to prevent transcription of the gene in target cells
XX
SQ Sequence 1110 BP; 328 A; 255 C; 263 G; 264 T; 0 U; 0 Other;

Query Match 71.9%; Score 798; DB 4; Length 1110;

Best Local Similarity 56.4%; Pred. No. 3.2e-194;

Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAGMGNNTATTTTGTNTATVACNTYNTATHGTGACNAAYTTTGYMSNTGNGAY 60
DB 1 ATGCACCGGCTCATCTTGTCTACACTTAATCTGGCAAACTTTTGACGCTGTGGAC 60
QY 61 ACNWSNCGNACNCCNCAWSNCCNWSNATHAAGCNTYTNMGNAAYGCAAYTTNMGNGN 120
DB 61 ACTTCTGCNAACCCCGCAGAGCGCATCATCAAGCTTTGCGCAAGCCCACTCAGGCGA 120
QY 121 GAYGARMNAAYCAAYTNAACGAYTTNTAYMNGMNGAYGACNAATCARGTNAARGN 180
DB 121 GATGAGAGCAATCACCCTCAGACTTGACGAGAGATGACCAATCCAGGTGAAGGA 180
QY 181 AAYGNTATGTTCARWSNCCNMGNTTCCNAAYMSNTAYCCNMGNAAYTNTYNTYNA 240
DB 181 AAGCGCTAGTGCAGAGTCTCTAGATTCCGGAACAGTACCAGAACTGCTCTGACA 240
QY 241 TGGMGNNTNCAWNSNCARGAARAAYCCNMGNATHCARNTGNTTGYAAYCAATTYGN 300
DB 241 TGGCGGCTTCACTCTCAGAGAAATACCGGATACAGTAGTGTGACATCATGTTTGA 300
QY 301 YTNGARARGCNGAARAAYATHTGYMNTAYGYTTCNTGAGTNGARAYTTHSN 360
DB 301 TTAGAGGAAGCAGAAATGATATCTGTAGTATGATTTTGTGAAGTGAATATATCC 360
QY 361 GABACWSNACNATHATHMNGNMGNTGTGYGNCAYAAARGATNCCNCGNATH 420
DB 361 GAACACAGACCTATTTAGAGAGAGATGCTGACACAGAAAGTCTCTCAAGATA 420
QY 421 AARWSNMGACNAAYCARATHAARATHACNTTAAARWSNGAYATYTTGYNCNAR 480
DB 421 AAATCAAGAACCAATTAATAATCAATTCAGTCCGATGACTACTTGTGCTAAA 480
QY 481 CCNGNTTYAARATHATYTAAYMSNTYNTYNGARAYTTCARCCNCGNCCNMSNGAR 540
DB 481 CCTGATTCMAATYATATCTTGTGGAAGATTTCCAAACCGCAGACCTTCAAG 540
QY 541 ACNAAYTGGGARGMNGTNAACNWSNMSNATHMSNGNMGNTMSTAYAAAYSNCCN 600
DB 541 ACCAACTGGGAATCTGTCAACAGCTTATTTCAAGGGTATCTTATAAATCTCTCATCAGTA 600
QY 601 ACNGAAYCCNACNTYNTATHGNCAYGNTNGAYAAARAATHGNCAGARTTYGAYACNGTN 660
DB 601 ACGGATCCCACTCTGATTTGCGATGCTGACAAAAAAATTGCGAATTTGATACAGTG 660
QY 661 GARGAYTNTYNTAATYATYTTAAAYCCNARGMSNTGGCARGAGAYTTNGARAAYATGAY 720
DB 661 GAAGATCTGCTCAAGTACTTCAATCCAGAGTCAAGCAAGAGATCTTGAGAAATATGAT 720
QY 721 YTNGAAYACNCGMGTAYMNGMNGMNTAYCAVGAAYGAARMSNARSTNGAYT 780
DB 721 CTGGACACCCCTCGGTATGAGGAGAGTATACATGACCGAAGTCAAAATTTAATCCTG 780
QY 781 GAYMGNNTYNTAAYGAYGACNAARMGNTAYMSNTGYACNCCNMGNAAYTAYMSNTNAY 840
DB 781 GATAGGCTCAATGATGATGTCAGAGGCTTACAGTTGCACTCCAGGAATTAATCTCGTCAAT 840

QY 841 ATTHMGNGARGARYNTAARYTNGCNAAYGTNGTNTTYYTCNMGNTGYTYNTNGNCAR 900
DB 841 ATTAGAGAGAGCTGAAGTGTGGCAATGTGTCTTTTCCAGCTGTGCTCTGTCAG 900
QY 901 MONTGYGNGNAAAYTGYGTGYGNCNCTNAAYTCGMSNMTGYACNTGYAAYMSN 960
DB 901 CGCTGTGAGGAAATYTGCTGTGGAACCTGTCACTGAGAGTCTTGCAATGCAATCA 960
QY 961 GGNABACNCTNABARATYACAGARGTNTNCARTTYGACNCGNCAVATHAARMGN 1020
DB 961 GGGAAACCTGGAAGAAAGATCATGAGTATTAACGTTGAGCTGGCCACATCAAGAG 1020
QY 1021 MNGNMGNGNCAARACNATGCTNMGNTNGAYATHCARNTNGAYCAVCAAGMNGTGY 1080
DB 1021 AGGGTAGAGCTAAGACCATGTGCTTACTTGTACATCCAGTTGATCCATGAAGATGC 1080
QY 1081 GAYTGATHTGYMSNMSNMGNCNCCNMG 1109
DB 1081 GATTGTATCTGACGCTCAAGACCACTCG 1109

RESULT 3

ACA64110 standard; DNA; 1110 BP.

ACA64110;

16-JUN-2003 (first entry)

Degenerate DNA sequence for ZVEGF4.

XX ds: growth factor homologue; ZVEGF4; proliferation; differentiation;
XX migration; mesenchymal cell; cell surface semaphorin; neuropilin;
XX cartilage development; T-cell; B-cell; rheumatoid arthritis; cancer;
XX autoimmune disease; inflammation; relinopathy; haemangioma;
XX ischaemic event; neuropathy; acute nerve damage; stroke;
XX central nervous system disease; peripheral nervous system disease.

OS Synthetic.

PN US6495668-B1.

PD 17-DEC-2002.

PF 03-MAY-2000; 2000US-00564595.

PR 03-MAY-1999; 99US-0132250P.

PR 10-NOV-1999; 99US-0164463P.

PR 04-FEB-2000; 2000US-0180169P.

PA (ZYMO) ZYMOGENETICS INC.

PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

DR WPI; 2003-352153/33.

PT Isolated growth factor analogue ZVEF4 proteins for pharmaceutical
PT composition as, e.g. therapeutic agents, diagnostic agents, and research
PT tools and reagents, includes polypeptides from amino acid residues.

PS Disclosure; Col 75-76; 67pp; English.

XX The invention relates to an isolated protein comprising a first
XX polypeptide disulphide-bonded to a second polypeptide. The first and
XX second polypeptides are from 113-138 amino acid residues and comprises
XX 258-370 amino acid residues of human growth factor homologue ZVEGF4. The
XX protein stimulates proliferation, differentiation, or migration of
XX mesenchymal cells and may modulate activities mediated by cell surface
XX semaphorins. ZVEGF4 may be used to design ant/agonists of neuropilin-
XX semaphorin interactions which may be of use in neurite growth,
XX cardiovascular development, cartilage and limb development, T- and B-cell

functions as well as treating rheumatoid arthritis, various forms of cancer, autoimmune diseases, inflammation, retinopathies, haemangiomas, ischaemic events, neuropathies, acute nerve damage, central nervous system diseases and peripheral nervous system diseases including stroke. The isolated protein is also used for a pharmaceutical composition as therapeutic agents, diagnostic agents, and research tools and reagents. It can be used in the study and regulation of cell and tissue development, as components of cell culture media. The proteins can form homodimers or heterodimers that act on tissues to control organ development by modulating cell proliferation, migration, differentiation, or metabolism. The gene for human ZVEGF4 is located on chromosome 11q22.3-23.1. The present sequence is a degenerate DNA sequence representing all possible sequences encoding ZVEGF4

Sequence 1110 BP; 215 A; 94 C; 178 G; 139 T; 0 U; 484 Other;

Query Match 71.9%; Score 798; DB 10; Length 1110;
Best Local Similarity 100.0%; Pred. No. 3.2e-194;
Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGCATGNTATTTTGTGTTATACNTATTTGTCNAATTTTGYGWSNTGNGNAY 60
DB 1 ATGCATGNTATTTTGTGTTATACNTATTTGTCNAATTTTGYGWSNTGNGNAY 60
QY 61 ACNWSNGCNAACNCNCAWSNCGNWSNATTAARGCNTTMMGNAAYGCAAYTTNMGNNGN 120
DB 61 ACNWSNGCNAACNCNCAWSNCGNWSNATTAARGCNTTMMGNAAYGCAAYTTNMGNNGN 120
QY 121 GAYGARSNAAYCAATTTNACNGATTTTATYMGNGGAYGARAANAHCARGTNAARGN 180
DB 121 GAYGARSNAAYCAATTTNACNGATTTTATYMGNGGAYGARAANAHCARGTNAARGN 180
QY 181 AAYGNTATGTCARWSNCCNMGNTTCCNAAYWSNTATCCMNGNAAYTTNTNTNACN 240
DB 181 AAYGNTATGTCARWSNCCNMGNTTCCNAAYWSNTATCCMNGNAAYTTNTNTNACN 240
QY 241 TCGMGNTTCAWNSNCARARAAYACMGNATHCARTTNTTGYAAYCARTTYG 300
DB 241 TCGMGNTTCAWNSNCARARAAYACMGNATHCARTTNTTGYAAYCARTTYG 300
QY 301 YTNNGARGCNGARARAAYATHTGYMNTAYGATTTGNTGAGTNGARAYATHTSN 360
DB 301 YTNNGARGCNGARARAAYATHTGYMNTAYGATTTGNTGAGTNGARAYATHTSN 360
QY 361 GARACWSNACNATHATHTMNGNMGNTGTTGYGNCAYARAGRTNCCNCGNATHT 420
DB 361 GARACWSNACNATHATHTMNGNMGNTGTTGYGNCAYARAGRTNCCNCGNATHT 420
QY 421 AARWSNMGACNAACARATHTAARATHTACNTTAAARWSNGAYGATTAATTTGTCNAAR 480
DB 421 AARWSNMGACNAACARATHTAARATHTACNTTAAARWSNGAYGATTAATTTGTCNAAR 480
QY 481 CCNGNTTAAARATHTAATTAAYWSNTTNTNGARGAYTTTCARCCNGCNGCWSNGAR 540
DB 481 CCNGNTTAAARATHTAATTAAYWSNTTNTNGARGAYTTTCARCCNGCNGCWSNGAR 540
QY 541 ACNAAITGGGARSNGTNAACWSNWSNATHTWSNGNMGNTSNTAAYAYWSNCCWSNGTN 600
DB 541 ACNAAITGGGARSNGTNAACWSNWSNATHTWSNGNMGNTSNTAAYAYWSNCCWSNGTN 600
QY 601 ACNGAYCCNACNTATHTGNCAGYGCNTNGAYARARATHGNCARTTGYAACNGTN 660
DB 601 ACNGAYCCNACNTATHTGNCAGYGCNTNGAYARARATHGNCARTTGYAACNGTN 660
QY 661 GARGAYTNTTAATTAATTAATTAAYCCNGARWSNTGGCARGARAYTTNGARAAATGTA 720
DB 661 GARGAYTNTTAATTAATTAATTAAYCCNGARWSNTGGCARGARAYTTNGARAAATGTA 720
QY 721 YTNAGAACNCCMGTTATMGNGGWSNNTAYCAYGAYMGNAAARWSNARGTNGAYTN 780
DB 721 YTNAGAACNCCMGTTATMGNGGWSNNTAYCAYGAYMGNAAARWSNARGTNGAYTN 780
QY 781 GAYMNTYNAAYGAYGAYCAARWGNTAYWSNTGYACNCCNMGNAAYTTAYWSNGTNAAY 840

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DB 781 GAYMNTYNAAYGAYGAYCAARWGNTAYWSNTGYACNCCNMGNAAYTTAYWSNGTNAAY 840
QY 841 ATHTMNGARGARYTNAAYTTGCAAAAGTNGTNTTTCNMGNTGYTNTTGTNCAR 900
DB 841 ATHTMNGARGARYTNAAYTTGCAAAAGTNGTNTTTCNMGNTGYTNTTGTNCAR 900
QY 901 MGNITGYGNGNAAAYTGAGTGYGNCACNGTNAAYTGCMGWSNTGYACNTGYAAW 960
DB 901 MGNITGYGNGNAAAYTGAGTGYGNCACNGTNAAYTGCMGWSNTGYACNTGYAAW 960
QY 961 GGNARAACNTNARAARATAYCAYGAGTNTTNCARTTYGARCNGCNGACAYATHAAMGN 1020
DB 961 GGNARAACNTNARAARATAYCAYGAGTNTTNCARTTYGARCNGCNGACAYATHAAMGN 1020
QY 1021 MNGNGMNGCNAARACNATGTCNTNGTNGAYATHTCARNTNGAYCAYGARGMNTGY 1080
DB 1021 MNGNGMNGCNAARACNATGTCNTNGTNGAYATHTCARNTNGAYCAYGARGMNTGY 1080
QY 1081 GAYTGYATHTGYWSNMGNCNCCNMG 1109
DB 1081 GAYTGYATHTGYWSNMGNCNCCNMG 1109

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RESULT 4

ADJ32759 standard; DNA, 1110 BP.

ADJ32759;

15-APR-2004 (first entry)

Human zvegf4 degenerate DNA.

Growth factor homologue; zvegf4; skin wound; venous stasis; ulcer; fracture repair; skin grafting; neovascularization; female reproductive tract disorder; bleeding; gastrointestinal tract; liver damage; hepatic chronic passive congestion; CPC; central haemorrhagic necrosis; CHN; neurite growth; neuropathy; neurodegenerative disease; multiple sclerosis; Alzheimer's disease; Parkinson's disease; cell proliferation; cancer; gene therapy; human; gene; ds.

Homo sapiens.

US2004002140-A1.

01-JAN-2004.

06-JUN-2001; 2001US-00876813.

03-MAY-1999; 99US-0132250P.

10-NOV-1999; 99US-0164433P.

04-FEB-2000; 2000US-0180169P.

03-MAY-2000; 2000US-00564595.

(GILB/) GILBERT T.

(HART/) HART C E.

(SHEP/) SHEPPARD P O.

(GILB/) GILBERTSON D G.

Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

WPI; 2004-070738/07.

New zvegf4 polypeptides and nucleic acids, useful for diagnosing or treating cell loss or abnormal cell proliferation, e.g. cancer, treating full-thickness skin wounds or treating female reproductive tract disorders.

Claim 34; SEQ ID NO 6; 73pp; English.

The invention relates to growth factor homologue zvegf4, its

corresponding nucleic acid and methods of using them. The sequences of the invention are used in the study and regulation of cell and tissue development, as components of cell culture media and as diagnostic agents. The zvegf4 polypeptide can be used in treating full-thickness skin wounds, including venous stasis, ulcers and other chronic, non-healing wounds, in fracture repair, skin grafting, in reconstructive surgery to promote neovascularisation and increase skin flap survival, to establish vascular networks in transplanted cells and tissues, or in treating female reproductive tract disorders, including acute or chronic placental insufficiency and prolonged bleeding. It can also be used to promote endothelialisation of vascular grafts and stents, in treating acute or chronic lesions of the gastrointestinal tract or treating or repairing liver damage. Zvegf4 can also be used for treating hepatic chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN). Zvegf4 proteins, agonists and antagonists can also be used to modulate neurite growth and development and demarcate nervous system structures. It can also be used for treating peripheral neuropathies or neurodegenerative diseases including multiple sclerosis, Alzheimer's disease or Parkinson's disease. The polypeptides, nucleic acids and antibodies can also be used to diagnose or treat disorders associated with cell loss or abnormal cell proliferation (including cancer). The invention is useful in gene therapy. The present sequence is human zvegf4 degenerate DNA.

Sequence 1110 BP; 215 A; 94 C; 178 G; 139 T; 0 U; 484 Other;

Query Match 71.9%; Score 798; DB 12; Length 1110;
Best Local Similarity 100.0%; Pred. No. 3.2e-194;
Matches 1109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCAVMGNTATTTTGTNTATYACNTYNTATHTGVCNAAYTTTGYMSNTGYMNGAY 60
1 ATGCAVMGNTATTTTGTNTATYACNTYNTATHTGVCNAAYTTTGYMSNTGYMNGAY 60
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61 ACNWSNGCNAACCCNCAWSNCCNWSNATHAARGCNYTMGNAAYGCAAAAYTTNMGNGN 120
121 GAYGARMSAAACAYTTTACNGAYTTNTATYMGNGMGAYGAAACNATHTCARGTNARGN 180
121 GAYGARMSAAACAYTTTACNGAYTTNTATYMGNGMGAYGAAACNATHTCARGTNARGN 180
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181 AAYGNTATGTCARMSNCCNMGNTTCCNAAVMSNTATCCNMGNAAYTTNTNTNACN 240
181 AAYGNTATGTCARMSNCCNMGNTTCCNAAVMSNTATCCNMGNAAYTTNTNTNACN 240
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241 TGGMGNTTTCAYWSNCCARGAARAACNMGNTATHTCARGTNTTGYAAYCARTTYGN 300
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241 TGGMGNTTTCAYWSNCCARGAARAACNMGNTATHTCARGTNTTGYAAYCARTTYGN 300
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361 GABAACMSNAACNATHATHTMGNGMGNTGTGYGNCAYAAARGATNCCNMGNAATH 420
361 GABAACMSNAACNATHATHTMGNGMGNTGTGTGYGNCAYAAARGATNCCNMGNAATH 420
361 GABAACMSNAACNATHATHTMGNGMGNTGTGTGYGNCAYAAARGATNCCNMGNAATH 420
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481 CCNGNTTAAAT 540
481 CCNGNTTAAAT 540
481 CCNGNTTAAAT 540
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781 GAYMNTYNTAAAYGAYGACNAAARMGNTATYMSNTGYACNCCMGNAATATAYMSNTNAY 840
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841 ATHMNGARGARATYNTAATYTGNCNAAYGNTGNTTATYTCNMGNTGYTNTYNTGNCAR 900
901 MONTGYGNGGNAAYTGYGNTGYGNAACNGTNAAYTGMGMSNTGYACNTGYAAYMSN 960
901 MONTGYGNGGNAAYTGYGNTGYGNAACNGTNAAYTGMGMSNTGYACNTGYAAYMSN 960
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1021 MNGNGMGNGCAARACNATGCGNTTNGTNGAYATHTCARNTMGAYCAVARGARMGNTGY 1080
1081 GAYTGYATHTGYMSNMSNMGNCNCCNMG 1109
1081 GAYTGYATHTGYMSNMSNMGNCNCCNMG 1109
1081 GAYTGYATHTGYMSNMSNMGNCNCCNMG 1109

RESULT 5
AAS04498
ID AAS04498 standard; DNA; 1728 BP.
AC AAS04498;
DT 07-SEP-2001 (first entry)
XX
DE Human PDGFD DNA.
XX
KW Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
KW VEGF-E; platelet derived growth factor; PDGF; FcTRX; hyperplasia; cancer;
KW neoplasia; anaemia; leucopenia; baldness; cardiovascular disorder;
KW fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
KW dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
KW inflammatory disorder; Graft versus host disease; coagulation; ds;
KW haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
KW multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
KW peripheral neuropathy; acute brain injury.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..205
FT /tag= b
FT /number= Exon 1
FT 82..1194
FT /tag= a
FT /product= "Human PDGFD"
FT 206..410
FT /tag= c
FT /number= Exon 2
FT 411..591
FT /tag= d
FT /number= Exon 3
FT 592..654
FT /tag= e
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FT 655..853
FT exon

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FT      /tag= f
FT      /number= Exon 5
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FT      854..1068
FT      /tag= g
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FT      exon
FT      1069..1178
FT      /tag= h
FT      /number= Exon 7
XX      MO200125437-A2.
XX      PD
XX      12-APR-2001.
XX      PF
XX      06-OCT-2000; 2000WO-US027671.
XX      PR
XX      07-OCT-1999; 99US-0158083P.
XX      13-OCT-1999; 99US-0159231P.
XX      PR
XX      04-JAN-2000; 2000US-0174485P.
XX      PR
XX      03-MAR-2000; 2000US-0186707P.
XX      PR
XX      10-MAR-2000; 2000US-0188250P.
XX      PR
XX      08-AUG-2000; 2000US-0223879P.
XX      PR
XX      12-SEP-2000; 2000US-00662783.
XX      PR
XX      20-SEP-2000; 2000US-0234082P.
XX      (CURA-) CURAGEN CORP.
XX      PA
XX      Shimkets RA, Lichenstein H, Hermann JL, Boldog FL, Minskoff S;
XX      PI
XX      Jeffers M;
XX      DR
XX      WPI; 2001-316172/33.
XX      P-PSDB; AA000704.
XX      PT
XX      Novel growth factor polypeptides termed as FCTR-X polypeptides, useful for
XX      treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
XX      wound healing and neuronal disorders.
XX      PS
XX      Disclosure; Fig 13; 171pp; English.
XX      CC
XX      The sequence represents DNA encoding a protein related to bone
XX      morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (VEGF
XX      -E) and platelet derived growth factor (PDGF). Polypeptides and
XX      CC
XX      polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as
XX      FCTR-X peptides and nucleic acids. FCTR-X proteins are useful for treating
XX      CC
XX      or preventing a disorder associated with aberrant expression, aberrant
XX      processing, or aberrant physiological interactions of the proteins in a
XX      CC
XX      mammal, where the disorder is characterised by insufficient or
XX      CC
XX      ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia.
XX      CC
XX      The peptides and their associated nucleic acids are useful for both
XX      CC
XX      promoting and inhibiting growth of cells and tissues and in treatment of
XX      CC
XX      cancer, anemia, leukopenia, baldness, for treating cardiovascular and
XX      CC
XX      fibrotic disorders, diabetic ulcers, obesity, infectious diseases,
XX      CC
XX      hyperproliferative and dysproliferative disorders, neurodegenerative
XX      CC
XX      disorders, osteoarthritis, inflammatory disorders, graft versus host
XX      CC
XX      disease, coagulation disorders such as haemophilia, and neural disorders
XX      CC
XX      including Parkinson's disease, Alzheimer's disease, multiple sclerosis,
XX      CC
XX      Huntington's disease, amyotrophic lateral sclerosis, peripheral
XX      CC
XX      neuropathy, acute brain injury and epilepsy
XX      SQ
XX      Sequence 1728 BP; 530 A; 364 C; 379 G; 455 T; 0 U; 0 Other;
SQ
Query Match 71.9%; Score 798; DB 4; Length 1728;
Best Local Similarity 56.4%; Pred. No. 4,4e-194;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
QY 1 ATGCAGMGNNTNATHTTGNTAATACNTATNATHTGCGNAAYTTTGYWNTGYMGNGAY 60
DB 82 ATGCACCGGCTCATCTTGTCTACACTCTAATCTCGCAACTTTTGAGAGCTGCGGAC 141
QY 61 ACNMGNGACNACNCCNARWNGCNMSNATTHAARGNTNMGNAAYGCAAYTTMGMNGN 120
DB 142 ACTTTCGACACCCCGACGAGCATCATCAAGCTTTGCGCAACGCCAAGCTCAGCGCA 201
QY 121 GAYGARWMSNAAYCAATTNACGAYTTNTAATGNNMGNGAYGARACNATTHCARGTNAARGN 180

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DB 202 GATGAGAGCAATCACCTTCACAGACTTGACCAAGATGAGACCATCCAGGTGAAGA 261
QY 181 AAYGNTATYGTNCARWNGCNMGNTTYCGNAAYWNTATCCNMGNAAYTTNTNTNACN 240
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QY 241 TGGMGNNTNCAWNSNCARBARAAVACNMGNAATHCARNTNGNTTGYAAAYCARTTYG 300
DB 322 TGGCGGCTTCACTCTCAGAGAAATTCACGAGATACAGTAGTGTGACATCAAGTTTGA 381
QY 301 YTNGARBARGNARAAAGATHTGWNNTATYATGATTTGNTGARNTNGARATHTWSN 360
DB 382 TTAGAGAGAGCAAGAAATGATATCTGATGATATATTTGGAAGTTGAAGATATATCC 441
QY 361 GARACNWSNACNATHTATMGNGMNGTGTGAGNCAYARAGRTNCCNMGNAATH 420
DB 442 GAATCCAGTACATATTTAGAGAGAGATGCTGTGACACAAAGAGTTCTCCCAAGATA 501
QY 421 AARWSNMGNAACNAAYCARATHTAATTAATTTAARWSNGAYATYATTTGTCNAAR 480
DB 502 AAATCAAGAGCAACCAATTAATCAATTCAGTCCGATGACTTGTGGCTAAA 561
QY 481 CCGGNTTYAARATHTTATYATWNTYTNNGARBARATTTGACRCNCGNCGNWSGAR 540
DB 562 CCGTGAATTCAGATTTATTTATTTCTTGTGAGATTTCCAAAGGAGAGCTTCAGAG 621
QY 541 ACNAAVTGGGARWNSGNTNACNWSNATHTWSNNGNTNMTAAYAAWNSNCCNWSGNT 600
DB 622 ACCAAGCTGGGAATGTGTCACAAAGCTTATTTCAAGGGTATCTTAATCTCCATCA 681
QY 601 ACNAGYCNACNNTNATHTGNGAGYNGNTNGAAYAAABAATHTGNCARTTYGAYACN 660
DB 682 ACGATTCCTCACTGATTTGGAGATGCTCTGACACAAAATTTGAGATTTGATACG 741
QY 721 YTNATYACNCCNMGNTATYMGNGMWSNTATYCAVAYGNAARWSNARNTNGAYTN 780
DB 802 CTGACACCCCTCGATATCAAGGACAGTCAATCAATGACCGAAGTCAAAAGTTGAC 861
QY 781 GAYGNTATNATYAGYAGYGCNAAARMGNTATWNTGYACNCCNMGNAAYTAYWSN 840
DB 862 GATAGCTCAATATGATATGCAAGCTTACAGTTGCACTCCAGAAATTAATCTGGTCA 921
QY 841 ATHTMGARBARATYTAATYTNMGNAAYGNTNTTATTTCCNMGNTGYTNTNGTCAR 900
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QY 1021 MNGNMGNGNCAARACNATGCGNTYTNNGNAYATHTCARNTNGAYCAVAYARMGNT 1080
DB 1102 AGGGGTGAGAGCTTAAGACATGCTTAAGTTGACATCACTGATGATCAATGAGAT 1161
QY 1081 GATYATHTGYWSNWSNMGNCNCCNMG 1109
DB 1162 GATTTATCTGACAGCTCAAGACCACTCG 1190

```

RESULT 6
 AAS04492
 ID AAS04492 standard; DNA; 1828 BP.
 XX
 AC AAS04492;

XX 07-SEP-2001 (first entry)
DT Human FCTR1 DNA present in clone 30664188.0.99.
XX
XX Bone morphogenetic protein-1; BMP-1; vascular endothelial growth factor;
XX VEGF-E; platelet derived growth factor; PDGF; FCTR1; hyperplasia; cancer;
XX neoplasia; anaemia; leukopenia; baldness; cardiovascular disorder;
XX fibrotic disorder; diabetic ulcer; obesity; hyperproliferation; human;
XX dysproliferation; neurodegenerative disorder; osteoarthritis; epilepsy;
XX inflammatory disorder; Graft versus host disease; coagulation; de;
XX haemophilia; neural disorder; Parkinson's disease; Alzheimer's disease;
XX multiple sclerosis; Huntington's disease; amyotrophic lateral sclerosis;
XX peripheral neuropathy; acute brain injury.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS /tag= a
XX /product= "Human FCTR1"
XX sig_peptide /tag= b
XX /tag= b
XX /tag= c
XX /product= "Mature human FCTR1"
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XX MO200125437-A2.
XX
XX 12-APR-2001.
XX
XX 06-OCT-2000; 2000MO-US027671.
XX
XX 07-OCT-1999; 99US-0158083P.
XX 13-OCT-1999; 99US-0159231P.
XX 04-JAN-2000; 2000US-0174485P.
XX 03-MAR-2000; 2000US-0186707P.
XX 10-MAR-2000; 2000US-0188250P.
XX 08-AUG-2000; 2000US-0223879P.
XX 12-SEP-2000; 2000US-0062783P.
XX 20-SEP-2000; 2000US-0234082P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Lichenstein H, Hermann JL, Boldog FL, Minskoff S;
XX Jeffers M;
XX WPI; 2001-316172/33.
XX P-PSDB; AAU0698.
XX
XX Novel growth factor polypeptides termed as FCTR1 polypeptides, useful for
XX treating cancer, cardiovascular and fibrotic diseases, diabetic ulcers,
XX wound healing and neuronal disorders.
XX
XX Claim 11; Page 11-12; 171pp; English.
XX
XX The sequence represents DNA encoding a protein related to bone
XX morphogenetic protein-1 (BMP-1), vascular endothelial growth factor (VEGF
XX -E) and platelet derived growth factor (PDGF). Polypeptides and
XX polynucleotides related to BMP-1, VEGF-E and PDGF are referred to as
XX FCTR1 polypeptides and nucleic acids. FCTR1 proteins are useful for treating
XX or preventing a disorder associated with aberrant expression, aberrant
XX processing, or aberrant physiological interactions of the proteins in a
XX mammal, where the disorder is characterized by insufficient or
XX ineffective growth of a cell or a tissue, e.g. hyperplasia or neoplasia.
XX The peptides and their associated nucleic acids are useful for both
XX promoting and inhibiting growth of cells and tissues and in treatment of
XX cancer, anemia, leukopenia, baldness, for treating cardiovascular and
XX fibrotic disorders, diabetic ulcers, obesity, infectious diseases,
XX hyperproliferative and dysproliferative disorders, neurodegenerative
XX disorders, osteoarthritis, inflammatory disorders, Graft versus host
XX disease, coagulation disorders such as haemophilia, and neural disorders
XX including Parkinson's disease, Alzheimer's disease, multiple sclerosis,

CC Huntington's disease, amyotrophic lateral sclerosis, peripheral
CC neuropathy, acute brain injury and epilepsy
XX
XX Sequence 1828 BP; 572 A; 380 C; 385 G; 491 T; 0 U; 0 Other;
SQ
Query Match 71.9%; Score 798; DB 4; Length 1828;
Best Local Similarity 56.4%; Pred. No. 4,6e-194;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
QY 1 ATGCATMGNTYTAATHTTGTNTATYACNTYNAHTTGCGCAATTTTGYSNNGMNGAY 60
DB 182 ATGCACCGGCTCATCTTGTCTTACACTTCAACTGCGCAACTTTTGACGCTGGGAC 241
QY 61 ACNMSNGCAACCCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 242 ACTTCTGCAACCCCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 301
QY 121 GAYGARWSNAAYCAVYTNACNGAYTTNTAYMNGMNGAYGARACNATHCARTNAARGN 180
DB 302 GATGAGAGCAATCACCTGCACAGCTTGACCGAAGATGAGACCATCCAGGTGAAGGA 361
QY 181 AAYGNTAYGTNCAKSNCCNMGNTTCCNAAVWSNTAYCCMGNAAVYTTNTYNAACN 240
DB 362 AAGGCTACGTGACAGTCTCTGATTCGCCAAGCTACCCAGGAACTGCTGCGACA 421
QY 241 TCGMGNTYTCAYWSNCAAGABAAYVACNMGNATHCARVNTGNTTGYAAYCARTTYG 300
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DB 602 AATTCAGAACGAAACCAATTTAATACATTCAGTACGATCTACTTGTGCTTAA 661
QY 481 CCNGNTYTAABATHTATYATVWSNTYTNGARAGATVYCARCNGCNGCNGMNGAR 540
DB 662 CCGATTCAGATTTATTTATTTCTTGTGGAAGNTTCCAAACCGGACGCTTCAAG 721
QY 541 ACNAAVTTGGATWSNCTNACNWSNMTATWSNNGNTWSTAYTAAYSNCCMNSGNT 600
DB 722 ACCAAGTGGAAATCTGTCAACAGCTCTATTTCAAGGGGTATCCATTAATCTCCATCAGTA 781
QY 601 ACNGAYCCNACNNTYATHTGCGNAGYGNNTYGAAYABAAATHCNGARTTYGACNGTN 660
DB 782 ACGGATCCACATCTGATTCGAGATGCTGCGCAAAAATTTGCAAAATTTATACAGTG 841
QY 661 GARGAYTNTAATATYATVYAYCCNGARWSNCTGACARGAYTTNGARAAVATGTAY 720
DB 842 GAAATCTGCTCAAGTACTTCAATCCAGAGTCATGCAAGAGATCTTGAGAAATGTAT 901
QY 721 YTNAGVACNCCMNGNTAYMNGMNSNTAYCAVAYMNAARWSNARTNGAYTNT 780
DB 902 CTGACACACCTCGGATGATGAGGAGGTCAATCCATGACCGGAAGTCAAAAATTTGACCTG 961
QY 781 GAYMNTYTAAGAYGAYCNAABMGNTAYMNTYACNCCMGNAAVYAYVSNNGNAY 840
DB 962 GATAGGCTCAAGATGATCCAAAGGCTTACATTCGACCTCCAGAAATTAATCTGGCAAT 1021
QY 841 ATTHMGARGARVTAATATYTNACNAYGNTGNTTATYTCNMNGTGYTNTNGTCAR 900
DB 1022 ATTAAGAGAGACTGAATTTGGCCAAATGTGCTTTTCCAGCTTCTGCTGAG 1081
QY 901 WNTYTGNGNAAATYTGCTGNTGNGNACNGTNAAYTGGMWSNTGTACNTGTAAVSN 960
DB 1082 CCTGTGGAGAAATTTGGCTGTGGAATCTGCACTGAGAGGTCTGTCACATGCAATTC 1141

QY	961	GGNARACNGNMAAATAATCAVAGARGNTYTCARITTYGARCCNGNCAYATHAPAKEN	1020
Db	1142	GGGAAAACCGTGAAAMAAATATCATGAGTATTAACAGTTTGAGCTGGCCACATCAAGAG	1201
QY	1021	MNGGSMNGCMAARACNATGGCANTTNGTNGAYATHCARRYNGAYCAVCAYGARMGNTGY	1080
Db	1202	AGGGGTAAAGTAAAGACCATGAGCTCTAATTGACATCCAGTTGATGATCAACATGAACGATGT	1261
QY	1081	GAYTGATHTGTWSNMSNMGNCCNCCNNG	1109
Db	1262	GATTTGATCTGACGCTCAAGACCAACTCTG	1290

RESULT 7
ABN84524
ID ABN84524 standard; cDNA; 1828 BP.

DT 21-OCT-2002 (first entry)

Human FCTR1 (platelet derived growth factor D) cDNA.

KM FCGR1; platelet derived growth factor D; PDGFD, human; Crohn's disease
 KM inflammatory bowel disease; gene therapy; antiinflammatory; vulnery;
 KM cyostatic; cardiovascular; gene; ss.

OS Homo sapiens.

Key	Location/Qualifiers
PH CDS	182. .1294

FT	big_peptide	182.550
FT		/*taq= b

PN WO200258716-A2.

PD 01-AUG-2002.

06-NOV-2001; 2001WO-US043846.

06-NOV-2000; 2000US-0246206P.

PA (CURA-) CURAGEN CORP.

Jeffers M, Shimkets RA, Prayaga S, Boldog FL, Yang M, Burgess CE;

DR WPI; 2002-599742/64.
DR P-PSDB; ABB79643.

PT Treating, delaying the onset of, or ameliorating an inflammatory
PT pathology (e.g. inflammatory bowel disease or Crohn's disease) by
PT administering to the subject fibroblast growth factors or a combination
PT of growth factors.

PS Disclosure; Page 19-21; 196pp; English.

The present sequence is that of cDNA clone J06654188.0.99 encoding human FCRL1, or placental derived growth factor 3 (PDGFD, see ABB75643). The clone was originally obtained from RNA from pituitary gland tissues, but FCRL1 RNA is also present in human uterine microvascular endothelial cells, erythroleukaemia cells, thyroid, small intestine, lymphocytes, adrenal gland and salivary gland. FCRL1 is a secreted protein that shows homology to human vascular endothelial growth factor E, and to human PDGF C, B and A. The invention provides cDNA and FCRL1 growth factors, polypeptides and variants, and polynucleotides encoding them, and methods of using these to treat, delay the onset of, or ameliorate, an inflammatory pathology, especially inflammatory bowel disease, a disease that occurs in the colon or small intestine, or Crohn's disease (all

CC claimed. The FGFCX and FCTRFX polypeptides and polymucosides are also
CC useful for treating growth and proliferative diseases such as cancer,
CC angiogenesis, collagen formation, fibrotic and cardiovascular diseases or
CC diabetic ulcers, and in wound healing. They can be used in screening and
CC detection methods, chromosome mapping, tissue typing, predictive
CC medicine, diagnostic assays, prognostic assays, and pharmacogenomics
XX
SQ Sequence 1828 BP, 572 A; 380 C; 385 G; 491 T; 0 U; 0 Other;

Sequence 1828 BP; 572 A; 380 C; 385 G; 491 T; 0 U; 0 Other;

Query Match	71.9%;	Score 798;	DB 6;	Length 1828;
-------------	--------	------------	-------	--------------

Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

1 ATGCAYMGNYTNATHHTTTCNTAYACNYTNATHTGGCNAAYTTTGTGWSNTGCMNGAY 60

Db 182 ATGCACCGGCTCATCTTGTCTACACTCTAATCGGCAACTTTGCAAGCTGTCGGGAC 241

61 ACNWSNGCNACNCNCARWSNGCNWSNATHARGCNYTNMGNA YGCNAAYTTNMGNGN 120

Db 242 ACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGCTTGGCGAACGCCAACCCTAGGCGA 301

QY 121 GAYGARWSNAYCAYYTNA¹CGAYYTNTAYMG²MGNGAYGARACNATHCARGTNAARGN 180

Db 302 GATGAGGCAATCACTCAGAGCTTGTACCGAAGAGATGAGACCATCTAGGTGAAGAAGCA 361

QY 181 AAYGNTAYGTNCARWSNCCMNGNTTYCCNAAYWSNTAYCCNMGNAAYVTNYTNYTNACN 340

D**b**

362 AACGCTACGTGCAGATCTTCAATTCCCGAACAAGTTAACCCAGGAACCTTCCTCCTGGAAAG

241 TGGMGNTNCAYWSNCARGAPAAACNMGNATHCARYTNGTNTTVCAYATVCCATTTTCCT 300

[illegible]

301 YTNGBAGBAGCNGABAAVGAATHTGCMGNTAVGAVTTCVCTNCABCTCNCABCTAVATTCAT 300

[illegible][illegible]

542

421 **A** **B** **C** **D** **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z** **aa** **ab** **ac** **ad** **ae** **af** **ag** **ah** **ai** **aj** **ak** **al** **am** **an** **ao** **ap** **aq** **ar** **as** **at** **au** **av** **aw** **ax** **ay** **az** **ba** **bb** **bc** **bd** **be** **bf** **bg** **bh** **bi** **bj** **bk** **bl** **bm** **bn** **bo** **bp** **bq** **br** **bs** **bt** **bu** **bv** **bw** **bx** **by** **bz** **ca** **cb** **cc** **cd** **ce** **cf** **cg** **ch** **ci** **cj** **ck** **cl** **cm** **cn** **co** **cp** **cq** **cr** **cs** **ct** **cu** **cv** **cw** **cx** **cy** **cz** **da** **db** **dc** **dd** **de** **df** **dg** **dh** **di** **dj** **dk** **dl** **dm** **dn** **do** **dp** **dq** **dr** **ds** **dt** **du** **dv** **dw** **dx** **dy** **dz** **ea** **eb** **ec** **ed** **ee** **ef** **eg** **eh** **ei** **ej** **ek** **el** **em** **en** **eo** **ep** **eq** **er** **es** **et** **eu** **ev** **ew** **ex** **ey** **ez** **fa** **fb** **fc** **fd** **fe** **ff** **fg** **fh** **fi** **fj** **fk** **fl** **fm** **fn** **fo** **fp** **fq** **fr** **fs** **ft** **fu** **fv** **fw** **fx** **fy** **fz** **ga** **gb** **gc** **gd** **ge** **gf** **gg** **gh** **gi** **gj** **gk** **gl** **gm** **gn** **go** **gp** **gq** **gr** **gs** **gt** **gu** **gv** **gw** **gx** **gy** **gz** **ha** **hb** **hc** **hd** **he** **hf** **hg** **hh** **hi** **hj** **hk** **hl** **hm** **hn** **ho** **hp** **hq** **hr** **hs** **ht** **hu** **hv** **hw** **hx** **hy** **hz** **ia** **ib** **ic** **id** **ie** **if** **ig** **ih** **ii** **ij** **ik** **il** **im** **in** **io** **ip** **iq** **ir** **is** **it** **iu** **iv** **iw** **ix** **iy** **iz** **ja** **jb** **jc** **jd** **je** **jf** **jj** **jh** **ji** **jj** **jk** **jl** **jm** **jn** **jo** **jp** **jq** **jr** **js** **jt** **ju** **jv** **jw** **jx** **ji** **jj** **jk** **jl** **jm** **jn** **jo** **jp** **jq** **jr** **js** **jt** **ju** **jv** **jw** **jx** **iy** **iz** **ka** **kb** **kc** **kd** **ke** **kf** **kg** **kh** **ki** **kj** **kk** **kl** **km** **kn** **ko** **kp** **kq** **kr** **ks** **kt** **ku** **kv** **kw** **kx** **ky** **kz** **la** **lb** **lc** **ld** **le** **lf** **lg** **lh** **li** **lj** **lk** **ll** **lm** **ln** **lo** **lp** **lq** **lr** **ls** **lt** **lu** **lv** **lw** **lx** **ly** **lz** **ma** **mb** **mc** **md** **me** **mf** **mg** **mh** **mi** **mj** **mk** **ml** **mm** **mn** **mo** **mp** **mq** **mr** **ms** **mt** **mu** **mv** **mw** **mx** **my** **mz** **na** **nb** **nc** **nd** **ne** **nf** **ng** **nh** **ni** **nj** **nk** **nl** **nm** **nn** **no** **np** **nq** **nr** **ns** **nt** **nu** **nv** **nw** **nx** **ny** **nz** **oa** **ob** **oc** **od** **oe** **of** **og** **oh** **oi** **oj** **ok** **ol** **om** **on** **oo** **op** **oq** **or** **os** **ot** **ou** **ov** **ow** **ox** **oy** **oz** **pa** **pb** **pc** **pd** **pe** **pf** **pg** **ph** **pi** **pj** **pk** **pl** **pm** **pn** **po** **pp** **pq** **pr** **ps** **pt** **pu** **pv** **pw** **px** **py** **pz** **qa** **qb** **qc** **qd** **qe** **qf** **qg** **qh** **qi** **qj** **qk** **ql** **qm** **qn** **qo** **qp** **qq** **qr** **qs** **qt** **qu** **qv** **qw** **qx** **qy** **qz** **ra** **rb** **rc** **rd** **re** **rf** **rg** **rh** **ri** **rj** **rk** **rl** **rm** **rn** **ro** **rp** **rq** **rr** **rs** **rt** **ru** **rv** **rw** **rx** **ry** **rz** **sa** **sb** **sc** **sd** **se** **sf** **sg** **sh** **si** **sj** **sk** **sl** **sm** **sn** **so** **sp** **sq** **sr** **ss** **st** **su** **sv** **sw** **sx** **sy** **sz** **ta** **tb** **tc** **td** **te** **tf** **tg** **th** **ti** **tj** **tk** **tl** **tm** **tn** **to** **tp** **tq** **tr** **ts** **tt** **tu** **tv** **tw** **tx** **ty** **tz** **ua** **ub** **uc** **ud** **ue** **uf** **ug** **uh** **ui** **uj** **uk** **ul** **um** **un** **uo** **up** **uq** **ur** **us** **ut** **uu** **uv** **uw** **ux**

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ID ADK18626 standard; DNA; 1828 BP.
XX
AC ADK18626;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human PDGF-D gene.
XX
KW de; gene; antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvael JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
DR New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 50; 255bp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a DNA used in the invention.
XX
SQ Sequence 1828 BP; 572 A; 380 C; 385 G; 491 T; 0 U; 0 Other;
Query Match 71.9%; Score 798; DB 10; Length 1828;
Best Local Similarity 56.4%; Pred. No. 4,6e-194;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
QY 1 ATGCAVNGYNTAHTTGTGTATTAACNTNATHTCGCAAAATTTTGTGWSNTGNGNGAY 60
DB 182 ATGCACCGGCTCATCTTGTCTACACTCTAATCTGCGCAACTTTTGGACGCTCGGGAC 241
QY 61 ACNWSNGCNAACCCGAGGCGCATCATCAAGCTTTGCCAAGCGCAACTCGAGCGA 120
DB 242 ACTTGTGCAACCCCGAGGCGCATCATCAAGCTTTGCCAAGCGCAACTCGAGCGA 301
QY 121 GAYGARMNAAYCAATYTTAATGATTTTATGNGNGNGAYGACACNATTCAGTNAARGN 180
DB 302 GATGAGACATCACTCACTCAAGATCTTGAACGAGATGAGACCATTCAGGTGAAGA 361
QY 181 AAYGNTYATGTCARWSNCCNMGNNTTTCNAAYWSNTATCCNMGNAAVYNTYNTYNA 240
DB 362 AACGCTACGTGAGAGCTCTAGATTTCCGCAACGCTACCCGAGAACCTGCTCTGACA 421
QY 241 TGGMNTYNTCAVWSNCGARPAAYACNMGNATTCARATYNTGNTTGYAAVCAATY 300
DB 422 TGGGGGCTTCACTCTCGAGAGATTAACGAGTACGATGTTTGAACATTCAGTTTGA 481
QY 301 YTNAGARGGCGNARAAAYATHTGNGNTATYATTTGTGNGARGNGARGAYATHTWSN 360
DB 482 TTAAGAGAGCAAAATGATATCTGTAGATATTTTGTGAAAGTTGAAGATATATCC 541

QY 361 GARACWSNACNATHTATMNGNNGNTGTGTGNGCAVYARAGRTCCNCCNMGNATH 420
DB 542 GAACCAATACATTAATAGAGAGAGTGTGACACAGAGAGTTCTCTCAAGATTA 601
QY 421 AARMSNMGACNAAYCABATTAATTAATTTAAATMSNGAYGATVATYTGNGCNAR 480
DB 602 AATCAAGAACGAAACCAATTAATCAATTCAGTCCGATGACTCTTGTGCTAA 661
QY 481 CCNNGNTTAAATATATATYATWSNTYNTNGARGATTTTCACNCCNCGNCCNMS 540
DB 662 CCTGATTCAGATTTATTTATTTCTTGTGGAAGTTTCCAAACCGAGAGCTTCA 721
QY 541 ACNAAVYTGGAARWSNNGTNAACNWSNATHTWSNNGTNTSNTATYAAVWSNCCN 600
DB 722 ACCAATCTGGAAATCTGTCAAGCTCTATTTCAAGGGATCTTAATCTCCATCA 781
QY 601 ACNGAYCCNACNNTATHTGNGAYGNTYTNAGVAAARAATHTGNGARTTYGAY 660
DB 782 ACGATCTCCACTCTGATTTGCGAGATCTCTGACAAATAATYGCAGAAATTTGA 841
QY 661 GARGAYNTNTAARTATYATTAAYCCNGARWSNTGCGARGARAYTTNGARAAVAT 720
DB 842 GAAGATCTGTCAAGTACTTCAATCCAGATCGACGCAAGATCTTGAGATATAT 901
QY 721 YTNAGAACNCCNMGNTATMNGNMGWSNTATYCAVYAGNAAARMSNAAAGTNGAY 780
DB 902 CTGACACCCCTCGTATTCAGAGGATCATACCATACCGGAAGTCAAAAGTTGAC 961
QY 781 GAVMNTYNAAYGAYGAGCAARMGNTATWSNTGYACNCCNMGNATYTWMSNGT 840
DB 962 GATAGGCTCATATATATATGACCAAGCTTACAGTTGACCTCCAGAAATHTCT 1021
QY 841 ATHTGNAARARATYNTAARTYNGCNAAVGTNGTNTYTYCCNMGNATGYTNTNG 900
DB 1022 ATTAAGAAAGAGCTGAAGTGTGCGCAATGTGCTTCTTCCAGTGTGCTCTCG 1081
QY 901 MGNITGNGNNAAYTGTGNTGNGNACNNGTAAATYTGNGMSNTGYACNTGYA 960
DB 1082 CGCTGTGAGAAATTTGTGCTGTGAACTGTAACCTGAGAGGCTGCGACATG 1141
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DB 1202 AGGGGTAGACCTTAGACCAATGCTTAGTTCATTCAGTTGATCAATCAATG 1261
QY 1081 GAYTGYATHTGYWSNMSNMGNCNCCNMG 1109
DB 1262 GATTGTATCTGACGCTCAAGACCACTCTCG 1290
RESULT 10
AAAS1541 ID AAAS1541 standard; cDNA; 1882 BP.
XX
AC AAAS1541;
XX
DT 26-SEP-2000 (first entry)
XX
DE SEQ. ID. 36 from WO0034474.
XX
KW Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; opthalmological; anti-rheumatic; anti-arthritic;
XX
XX vulnerable; ss.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers

[illegible]

Dd		406	AACGGCTAACGTGCAAGATGCTTCAAGTTCCCGAACAACGTACCACCAAGAACCCTGCTCCTAC	465
Oy		241	TGAGMNTYNCAYWSNCRGARBAAYACNMGNATHCARVTNGTNTTYGAVAACATPYG	300
Dd		466	TGGCGGCTTCACTCTCAGAGAAATACACGGATACAGCTAGTGTTGCACATCACGTTTGA	525
Oy		301	YTNGARGARCGNGBARAYGAATHTGTMGNTAYCATYTTGTNGARGTNGARGAVATHMSN	360
Dd		526	TTAAGAGGAAGCAAAAATGATATCTGTAAGGTATGATATTGTGGAAAGTTGAAGATATATCC	585
Oy		361	GABACNMSNAANAATHATMGNGMMNTGGTGYGANCAYABARGRTNCCNCGMNATH	420
Dd		586	GAAACCMGTCATTTATTTAGAGACGATGGTGTGACACAGGAAGTTCCTCCAGAGATA	645
Oy		421	AARSMNMGNAANAAVCARATTHAETHACNTTYAARWSNGAYGYATYTTYGTNGCAAR	480
Dd		646	AAATCAAGAACGAACCAATTTAAATCACAATTCAGTCCGATGACTACTTTGTGGCTPAA	705
Oy		481	CCNGANTTYAARATHIATVATWSTYNTYNTNGARGAYTTCARCNCNCGNCGNMSGAR	540
Dd		706	CCTGATTCACAAGATTTATTTATCTTCTCTGGAMAATTTCCAAACCCGAGCAGCTTCAGAG	765
Oy		541	ACNAAYTGGGARMNGTNACNWSMNSUATHSNSNGNTNNTYAAVYMSCCNWSNGTN	600
Dd		766	ACCACTTGGGAATCTGTCCACAAGCTCTATTTTTCAAGGGGATCTCTATTACTCTCCATCGTA	825
Oy		601	ACNGAYCCMACNTYNATHGNCNGAIGCNVTNGAVYABAARATHGNCGARTTYGAYACG	660
Dd		826	ACGGATCCCACTCTGATTTGCCGAGTGCCTCTGACCAAAAAAATYGAGAAITTTGATACG	885
Oy		661	GARGAYTNTYNAARFVATVTTYAAVCCNGARMSNTGGCARGARAYYTNGARBAVATGTAY	720
Dd		886	GAAATCTGCTCAAGTACTTCAATCCAGAGTCATGCGAAGAAAGATCTTGAGAAATATGTAT	945
Oy		721	YTNGAYVCCNCGMNTAYMGNGMMGMMSNTAYCAYAMGNABRMSNAARGTNGAYTN	780
Dd		946	CTGACACCCCTCGGTATCGAGGCAAGGTCAATACATACCGGAAGTCAAAAAGTTGACCTG	1005
Oy		781	GAYMNTYNAAYGAYGAYGACNAARMGNTAYVSNSTGYACNCCNMGNAAYVYASNGTNAAY	840
Dd		1006	GATAGCTCAATGATGATGCTCCAAACGCTTACAGTTGCACCTCCAGGAATTTACTCGGTCAAT	1065
Oy		841	ATHMNGARGARVYTNAAARYTNGCNAAYGVINGTNTYTTCCNMGNTGYTYNTNGTCAR	900
Dd		1066	ATAAGAGAAGAGCTGAAGTTGGCCAATGTGGTCTTTCTTCCACGTTGCTCTCGTGCAG	1125
Oy		901	MGNTGYGNGNAAVYTGCVNTGYGNAACNGTNAAYTGGMNSMTGYACNTTGYAATWSN	960
Dd		1126	CGCTGTGGAGAAATTTGTGCTGTGGAACGTCTCAACTGAGAGTCTCTCACATGCAATTTCA	1185
Oy		961	GSNABACNGTNAARAARTAYCAVAGRGIVYTNCAATTTYGARCCNGNCAVATHAEMGN	1020
Dd		1186	GGGAAAAACCTGAAAAAGTATCATGAGGTATTTACAGTTTAGCTGGCCACATCAAGAGG	1245
Oy		1021	MGNMGNMGNCNAAPACNATGGCNYTNGTNGAVATHCARVTNGAYCAVYAGRMENPTY	1080
Dd		1246	AGGGGTAGAGTAAAGACCATGGCTCTAGTGGATCATTCAGTTGATCAACATGAACGATGC	1305
Oy		1081	GATYGTATHTGYMSMSMNGNCCNMG	1109
Dd		1306	GATGTATCTGACGCTCAAGACCACTCG	1334
<hr/>				
RESULT 11				
AAC81555				
ID	AAC81555 standard; cdna; 1882 BP.			
XX	AAC81555;			
XX	AC			
XX	09-MAR-2001 (first entry)			
DE	Human growth factor homologue zvegf4 cDNA, SEQ ID NO:1.			

ID	AAH47772	standard; cDNA; 1882 BP.
XX	AAH47772;	
AC	07-JAN-2002	(first entry)
DT	Human zvegf4 polypeptide encoding cDNA.	
XX		
DE	Zvegf4; bone; ligament; cartilage; osteoblast; osteoclast; chondrocyte;	
XX	bone cancer; osteonclerosis; bone defect; osteogenesis; osteoporosis;	
KM	osteopathic; vulnery; human; ss.	
XX		
OS	Homo sapiens.	
XX		
TH	Key	Location/Qualifiers
FT	CDS	226..1338
FT		/*tag= a
FT	sig_peptide	/product= "zvegf4 protein"
FT		226..279
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FT	mat_peptide	/note= "secretory peptide"
FT		280..1335
FT		/*tag= c
XX		
PN	WO200157083-A1.	
XX		
PD	09-AUG-2001.	
XX		
PF	03-MAY-2000; 2000MO-US012095.	
XX		
PR	04-FEB-2000; 2000US--0180169P.	
XX	31-MAR-2000; 2000US--00540224.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Gilbertson DG, Hart CE;	
XX		
DR	WPI; 2001-611088/70.	
XX	P-PSDB; AAG65601.	
PT		
PT	Use of zvegf4 polypeptide for promoting bone, ligament or cartilage	
PT	growth in mammal at site of fracture, implant, and bone graft, and for	
PT	promoting growth or differentiation of osteoblasts, chondrocytes in	
PT	culture.	
PS		
XX	Example 1; Page 44-47; 57pp; English.	
XX		
CC	The invention relates to the use of zvegf4 polypeptide for promoting	
CC	bone, ligament or cartilage growth in a mammal, and for promoting	
CC	proliferation or differentiation of osteoblasts, osteoclasts,	
CC	chondrocytes or bone marrow stem cells in culture. For promoting	
CC	cartilage growth, chondrocytes are cultured ex vivo in presence of the	
CC	zvegf4 polypeptide and then placed into mammal where cartilage is to be	
CC	grown. Zvegf4 polypeptide is useful for promoting growth of bone,	
CC	ligament or cartilage in a mammal at a site of bony defect such as	
CC	fracture, bone graft, implant or periodontal pocket, in humans and non-	
CC	human animals such as domestic animals including livestock and companion	
CC	animals. Zvegf4 is used for promoting growth of bone, ligament, or	
CC	cartilage in conditions of bone defects following therapeutic treatments	
CC	of bone cancers or other conditions characterized by increased bone loss	
CC	or decreased bone formation, or elevation of peak bone mass in pre-	
CC	menopausal woman. It is also useful for healing bone following radiation	
CC	-induced osteonecrosis, repairing bone defects arising from surgery, and	
CC	promotion of bone healing in plastic surgery, increasing bone formation	
CC	during distraction osteogenesis, treating bone injuries including repair	
CC	of cartilage and ligament and treatment of osteoporosis. The present	
CC	sequence represents a human zvegf4 polypeptide encoding cDNA	
XX		
SQ	Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 U; 0 Other;	
XX		
Query March	71.9%; Score 798; DB 4; Length 1882;	
Beet Local Similarity	56.4%; Pred. No. 4,7e-194;	
Matches 626; Conservative 300; Mismatches 183; Indels	0; Gaps	0

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Db	226	ATGCACGGGCTCATCTTTGTCTACACTTAATCTGCGAAACTTTTGACGCTGTGGGAC	285
QY	61	ACMNSNGCNA CNCCNCARWSNCGCWNWSNATHARGCNTYTMGNAAYGCNAAAYTYTMNGMN	120
Db	286	ACTTCTGCAACCCCGCAGAGCGCATCCATCAAGAGTTTGCCCAACGCCCACTCAGGCGA	345
QY	121	GATGARSNNAKYCAVYTNACNGAYTTNTAYMGMNGNAYGARACNAHTCAGTNAARGN	180
Db	346	GATGAGGCAATYACCTCACAAGACTTGTACGGAAGAGYAGACCATCCAGGTGAAGA	405
QY	181	AAYGNTAYGTNCARWSNCCNMGNTTYCCNAAYSNTAYCCNMGNAAYTYTYNTYNA CN	240
Db	406	AAACGGCTACGTGACAGAGTCTTAAGNTTCCGAAACAGCTACCCACAGAACCTGTCTGACA	465
QY	241	TGCMGNTYTNCAWNSCARGAPAAVACMNGNATHCARVYNTGNTTYGAYAAVCAPTTYGN	300
Db	466	TGGCGGCTTCACTCTCAGGAAATAACGGATAACGTAAGTGTGTGAACAATCAGTTTGA	525
QY	301	YTNARGARGCNGARAAVGAVHTHGYMGNATYGAVYTYTGNTGARGTNGARGAYVTHMSN	360
Db	526	TTAAGGAGAGAAATGATATCTGATGATGATTTTGTGGAAATTGAAATATATCC	585
QY	361	GARACNWSNACNATHATHMNGMNGMTGTGTGYGNCAYARGATNCCNCCMGNATH	420
Db	586	GAACCCAGTACCATTTATTAAGAGACGATGTGTGACACAAGAAAGTTCTCTCAAGATA	645
QY	421	AARBSNMGNAACNAAYCARATHAARATHACNTTYAARBSNAGVATATYTYGTNCNAR	480
Db	646	AAATCAAGAAAGAACCAAAATTTAAATCATTCACATTCAGATGATCTGTGTGTGCTTAA	705
QY	481	CCNGANTTYAARHTHTAYTWSVYTYNTYNGARGAYTYTCARCCNGCNGCNSNGAR	540
Db	706	CTGTGATTCAGATTTATTTATTTCTTGTGTGAAGATTTCCAAACCCGACAGCTTCAGAG	765
QY	541	ACNAAVYTGGRWSNGTNACNWSWSNATHWSNNGSGNTMSNTAYAAVWSNCNWSNGTN	600
Db	766	ACCAACTGGGAAATCTGTCAACAAGCTCTATTTCCAGGGGATCTCTAATACCTCCACAGTA	825
QY	601	ACNAYCCNNA CNYTNATHGNCNAGVANCYTNAGVABAARATHGNCAGATTTGAYVNCNTN	660
Db	826	ACGAGTCCCATCTGATTTGCGGATGCTTGACACAAAATAATTCAGAAATTTGATCAAGTG	885
QY	661	GARGAYTYNTYNAARATAYTYTAAYCCNGARWSNTGGCARGARAYYTNGARAAVATGAY	720
Db	886	GAAGATCTGTCAAGTACTTCAATCCAGATGCATGCGCAAGAAGATCTTGAGAAATATGAT	945
QY	721	YTNAYVACNCCMMENTAYMNGNCGMNGMNSNTAYCAVYAMENAAARMSNAAGTNAAYTN	780
Db	946	CTGACACACCTCTGGTATCGAGGACGATCAATACATGACGGAAGTCAAAAGTTGACCTG	1005
QY	781	GAYVGNNTYNAAYGAYVGCNAAAHMGNATYVSNSTGYACNCCMNGAAATYAVWSNNTNAY	840
Db	1006	GATAGGCTCAATGATGATGCCAACGTTTACAGTTGCACTCCACAGAAATTACTCGGTCAAT	1065
QY	841	ATHMNGARGARVYTNAAVYTYNGCNAAYGTNGTNTTYTYCCNMGTGYTYTYNTGNTCAR	900
Db	1066	ATAAGAGAGAGCTGAAAGTTGGCCAAATGTGTCTTCTTCCACGTTGCTCTCTCGTGACG	1125
QY	901	MGNTYGSGNGNAAVYTGVCNTGYGNCNACNTNAAVYTGGMNMSYTGACNTGYAAVMSN	960
Db	1126	CGCTGTGAGGAAATGTGGCTGTGGAACTGTCAACTGAGAGTCTCTGCACTGCAATYCA	1185
QY	961	GNNAARACNGTNAARAAATAYCAVARGATYTNCAATTYGARCCNGNCAYATHAARMGN	1020
Db	1186	GGGAAACCCGTGAAAAAGTATCATGAGGTATTAACGTTTGAAGCTGCGCAATCAAGAGG	1245
QY	1021	MGNMNGMNGCNAARACNATGGCNYTNGTNTNAYATHCARVYTNNGAYCAVYAGABMGNTGY	1080
Db	1246	AGGGTGTGAAGTAAAGACATGGCTCTTAATTACATCCAGTTTGATCACCATGAAAGATGC	1305

Oy		781	GAYWGNNTNNAAYGAGVAGCNAAABMGTAAYWSNTGYACNCCMGAAATTAAYWSNGTNAAY	840
Db		1006	GATWGGCTCAATGATGATGCACAAGCGTTAAGTGACTGCCACCAGAATTACTCGGTCAAT	1065
Oy		841	ATHMNGARGARYTNNAARYTNGCNAAYGTNGINTTYTTYCCNMGNTGYTYTYVTNGTCAR	900
Db		1066	ATAAGAGAAGAGCTGAAGTAGTTGGCCAATGTGGCTTTCTTCCACGTTGGCTCTCGTGCAG	1125
Oy		901	MGNTGYGGNGNNAAYTGYGNTGYGNNACNGTNAAYTGMGNWSNTGYACNTGYAAYWSN	960
Db		1126	CGCTGTGGAGGAATTTGTGGCTGTGGAACGTGCAACTGGAAGTCTCTGCACATGCATTC	1185
Oy		961	GGNAAPACNGNNAABAARTYACAYABCTNYTNCARTTYGARCCNGGNCAYATTAABMN	1020
Db		1186	GGGAAAACCGTGA AAAAAGATATCATAGATATTACGTTTGAGCTGGCCACATCAAAGGG	1245
Oy		1021	MGNMGNNMGNGNNAARACNATGCANTYTNGAYATHCARYTNGAYCAYCAYGABMGNTGY	1080
Db		1246	AGGGGTAGAGCTTAAGACCATGGCTCTTAATTGACATCCAGTTGGATCACCATGAAGATGC	1305
Oy		1081	GAYTGYATHTGTYSWNSWMSNMCNCNMG	1109
Db		1306	GATTGTATCTGCAGCTCAAGACCAACTCTG	1334
RESULT 14				
ABNB84420	ID	ABNB84420	standard; cDNA; 1882 BP.	
XX	AC	ABNB84420;		
XX	DT	21-OCT-2002	(first entry)	
XX	DE	Human zvegfg4 cDNA.		
XX	KM	Zvegfg4; human; kidney; acute tubular necrosis; nephrotropic;		
XX	KW	gene therapy; gene; 5b.		
XX	OS	Homo sapiens.		
FH	Key	Location/Qualifiers		
FT	CDS	226..1338		
FT		/tag= a		
FT	sig_peptide	/product= "zvegfg4"		
FT		226..279		
FT	mat_peptide	/tag= b		
FT		280..1335		
FT		/tag= b		
XX	PN	WO200260467-A2.		
XX	PD	08-AUG-2002.		
XX	PP	26-OCT-2001; 2001WO-US050155.		
XX	PR	30-OCT-2000; 2000US-0244479P.		
XX	PA	(ZYMO) ZYMOGENETICS INC.		
XX	PI	Hart CE, Topouzis S;		
XX	DR	WPI; 2002-590847/63.		
XX	P	P-PSDB; ABB79588.		
XX	FT	Improving kidney function, or enhancing proliferation or survival of		
XX	FT	kidney tubule epithelial cells or epithelial cell precursors in a mammal		
XX	FT	comprises administering a zvegfg4 protein or zvegfg4 protein-encoding		
XX	FT	polynucleotide.		
XX	PS	Example 1; Page 35-38; 45pp; English.		
CC	CC	The present sequence is that of cDNA encoding human zvegfg4, a protein		
CC	CC	which activates the alpha-alpha, alpha-beta and beta-beta forms of the		

[illegible]

```
OY 721 YTNAGAYACNCCNMGTNGMNGMNSNTAYCAYAGMNGMNAARSGTNGAYTNN 780
DB 946 CTGAGACACCCCTCGGTATCGAGGAGGTCAATACCGAAGTCAAAAGTTGACCTG 1005
OY 781 GAYMGNNTNAYAGAYAGMNGMNAARSGTNGAYTNN 840
DB 1006 GATAGGCTCATATGATGATGCGAAGCGTTACAGTTGACCTCCAGAAATCTCGGCAAT 1065
OY 841 ATTMNGNBARATNTNARNTNGMNAAYGNTGNTTNTTTCNNNGTGYTNTNTGNCAR 900
DB 1066 ATAGAGAAAGAGCTGGAAGTTGGCCAAATGCTCTTCTTCCAGTTGCCCTCCGAGCAG 1125
OY 901 MGNTRYGNGMNAAYTGYGNTGYGNAACNGTNAAYTGGMNGMNSNTAYCAYAGMNGM 960
DB 1126 CGGTGAGAGAAATGTTGCTGTGGAACGTCACTGAGAGTCTGCGACATCAATCA 1185
OY 961 GGNAAACNCTNAAARATRYCAYAGRTNTNCAATYTGARCCNGMNGMNAAYTHAARMGN 1020
DB 1186 GGGAAAAACCGTGAAGAAAGTATCATGAGTATACAGTTGAGCTGGCCACATCAAGAGG 1245
OY 1021 MNGMNGMNGMNAARACNATGSCNTNGTNGAYATHCATYNGAYCAYAGMNGMNTGY 1080
DB 1246 AGGGGTAGAGCTTAAGACCATGCTTGAATGACATCCAGTTGATCAGATGAAGATGC 1305
OY 1081 GAYTGYATHTGYMNSMNGMNGMNGMNG 1109
DB 1306 GATTGTATCTGACGCTCAAGACCACTCG 1334

RESULT 15
ABO73239
ID ABO73239 standard; cDNA; 1882 BP.
AC ABO73239;
XX
XX
XX 30-SEP-2002 (first entry)
DE Human zvegf4 encoding cDNA SEQ ID NO:1.
XX
XX Human; zvegf4; cell proliferation; extracellular matrix production;
XX fibroproliferative disorder; PDGF-D; platelet derived growth factor;
XX PDGF; vascular endothelial growth factor; VEGF; cytosolic; nephrotropic;
XX hepatotropic; antiinflammatory; osteopathic; antiarthritic; metastasis;
XX prostate tumour; prostate cancer; glomerulonephritis; lupus nephritis;
XX diabetic tumour; osteosclerosis; renal arteriosclerosis; nephrotic syndrome;
XX chronic active hepatitis; cirrhosis; osteopetrosis; osteosclerosis;
XX hyperostosis; osteoarthritis; gene; 88.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 226..1338
XX FT /*tag= a
XX FT /product= "zvegf4"
XX
XX US2002064832-A1.
PD 30-MAY-2002.
XX
XX 14-MAR-2001; 2001US-00808972.
PF
XX 03-MAY-1999; 99US-0133250P.
XX 10-NOV-1999; 99US-0164463P.
XX 04-FEB-2000; 2000US-0180169P.
XX 03-MAY-2000; 2000US-0056459S.
XX 26-SEP-2000; 2000US-0235295P.
XX
XX (HART/) HART C E.
XX PA (TOPO/) TOPOLUIS S.
XX PA (GILB/) GILBERTSON D G.
XX
XX Hart CE, Topoluis S, Gilbertson DG;
```

```
XX
XX WPI: 2002-573696/61.
XX DR P-PSDB; ABB51640.
XX
XX PT Reducing proliferation or extracellular matrix production by a cell in a
XX PT mammal, useful for treating fibroproliferative disorders of bone, liver
XX PT and kidney, comprises administering a zvegf4 antagonist.
XX
XX Example 1; Page 18-19; 34pp; English.
XX
XX The present invention describes a method for reducing proliferation of or
XX extracellular matrix production by a cell in a mammal. The method
XX comprises administering to the mammal a composition comprising a
XX therapeutically effective amount of a zvegf4 antagonist chosen from anti-
XX zvegf4 antibodies, inhibitory polynucleotides, inhibitors of zvegf4
XX activation, and mitogenically inactive, receptor-binding variants of
XX zvegf4. Zvegf4 (also called PDGF-D) is a multi-domain protein that is
XX structurally related to platelet derived growth factor (PDGF) and
XX vascular endothelial growth factors (VEGF). Zvegf4 has cytostatic,
XX nephrotropic, hepatotropic, antiinflammatory, osteopathic and
XX antiarthritic activities. The method is useful for reducing proliferation
XX of mesangial, epithelial, endothelial, smooth muscle, fibroblast,
XX osteoblast, osteoclast, neuronal, stromal, stellate or interstitial cells
XX in a mammal, in particular proliferation of prostate tumour cells, and
XX for reducing extracellular matrix production by a cell in a mammal
XX suffering from a fibroproliferative disorder of kidney, bone or liver. In
XX particular it is useful for reducing metastasis of prostate cancer cells to bone in a
XX mammal and for treating a fibroproliferative disorder of kidney, liver or
XX bone in a mammal. Fibroproliferative disorders of the kidney include,
XX CC glomerulonephritis, diabetic glomerulosclerosis, lupus nephritis, renal
XX arteriosclerosis and nephrotic syndrome, disorders of the liver include
XX chronic active hepatitis and many other types of cirrhosis, and disorders
XX of the bone include osteopetrosis, hyperostosis, osteosclerosis,
XX osteoarthritis, and ectopic bone formation in metastatic prostate cancer.
XX The present sequence encodes human zvegf4, which is used in an example
XX from the present invention
XX
XX Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 U; 0 Other:
XX
XX Query Match 71.9%; Score 798; DB 6; Length 1882;
XX Best Local Similarity 56.4%; Pred. No. 4,7e-194;
XX Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
OY 1 ATGCAVGNNTNATHTTGTGNTTAYACNNTATHTGVCNAAATTTGYMNSMNGMNGAY 60
DB 226 ATGCAACCGGTCAATCTTGTCTACCTCTTAATCTGCGAAGCTTTCGAGCTGTCGGGAC 285
OY 61 ACNWSMNCNACNCCNCAWSMNGMNSMNAATHAARGCNYTNMGNAAVGCNAAAYTNNMNGMGN 120
DB 286 ACTTCTGCAACCCCGAGAGCGCATCATCAAGCTTTCGGAAGCCCAACCTCAAGGCA 345
OY 121 GAYGARMNSNAAVAYTNNACNAYTNTAYMNGMNGAYGARAACNATHTCARGTNNAARGN 180
DB 346 GATGAGAGCAATCACTCAAGACCTTGATCCGAAGAGAACCAATCAAGGTGGAAGGA 405
OY 181 AAYGNTAYGTNCAFWNSCCNMGNNTTCCNAAVWSNTAYCCMNGNAAAYTNTNTNACN 240
DB 406 AACGCTAGCTGAGAGTCTCTAGATTCCGGAACAGTACCCAGAACCTGCTCTGACA 465
OY 241 TCGMGNNTNAYMNSNCARARAAYACNMGATHTCARNTNTTGYGAYAAVCAATTYGNGN 300
DB 466 TGGCGGCTTCACTCTCAAGAGAAATACCGATACAGCTAGTGTGACAAATCAATGTTGGA 525
OY 301 YTNAGARGCNGARARAAYATHTGNGMNTYGYATYTTGNTGARGCTNGARAYATHMSN 360
DB 526 TTAGAGAGAGCAAGAAATATATCTGTAGTATGATTTTGTGGAAGTTGAAGATATATCC 585
OY 361 GARACNWSNACNATHTATMNGMNGMNGTGTGYGNCAYAAARGAGTNCNCCNMGNATH 420
DB 586 GAACACAGTACCATATATAGAGAGCATGAGTGTGACACAGGAAGTTCTCCAGAGATA 645
OY 421 AARMSMNGMNAAYCAATHTAARATHTACNTTAAARMSNGAYGATATYTTGTGNCNAAR 480
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:27:55 ; Search time 7947.09 Seconds
(without alignment)
6605.133 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
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6: gb_pat:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798	71.9	1110	6	BD276212 GROWTH PA
2	798	71.9	1110	6	AR267254 Sequence
3	798	71.9	1110	6	AX044492 Sequence
4	798	71.9	1428	9	AB033832 Homo sapi
5	798	71.9	1828	6	AX164744 Sequence
6	798	71.9	1828	6	AX664403 Sequence
7	798	71.9	1828	6	AX704461 Sequence
8	798	71.9	1828	6	AF335584 Homo sapi
9	798	71.9	1882	6	BD264400 Homo sapi
10	798	71.9	1882	6	BD276211 GROWTH PA
11	798	71.9	1882	6	AR238015 Sequence
12	798	71.9	1882	6	AR267253 Sequence
13	798	71.9	1882	6	AR282980 Sequence
14	798	71.9	1882	6	AR404883 Sequence
15	798	71.9	1882	6	AX044487 Sequence
16	798	71.9	1882	6	AX207483 Sequence
17	798	71.9	1882	6	AX574390 Sequence
18	798	71.9	2253	6	BD267598 Platelet-
19	798	71.9	2253	6	AR487713 Sequence

20	798	71.9	2253	6	AX739932 Sequence
21	798	71.9	2253	9	AF336376 Homo sapi
22	798	71.9	3729	9	AY027517 Homo sapi
23	798	71.9	3736	6	AX365305 Sequence
24	782	70.5	1734	6	AX164761 Sequence
25	782	70.5	1734	6	AX704478 Sequence
26	757.4	68.2	1162	6	AX454728 Sequence
27	757.4	68.2	1162	6	AX464052 Sequence
28	757.4	68.2	1162	6	AX491206 Sequence
29	757.4	68.2	1162	9	AX359116 Homo sapi
30	757.4	68.2	3710	9	AY027518 Homo sapi
31	757.4	68.2	3718	6	AX365307 Sequence
32	757.4	68.2	4065	9	BC030645 Homo sapi
33	720.8	64.9	1343	10	AB052170 Rattnu no
34	714.8	64.4	1113	6	AX164748 Sequence
35	714.8	64.4	1113	6	AX664407 Sequence
36	714.8	64.4	1113	6	AX704465 Sequence
37	714.8	64.4	1113	10	AF335583 Mus muscu
38	714.8	64.4	1472	6	BD276252 GROWTH PA
39	714.8	64.4	1472	6	AR238016 Sequence
40	714.8	64.4	1472	6	AR267294 Sequence
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ALIGNMENTS

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DEFINITION	BD276212				
ACCESSION	BD276212.1	GI:33085980			
VERSION	JP 2002542825-A/2.				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 1110)				
AUTHORS	Sheppard,P.O., Hart,C.E., Gilbert,T. and Gilbertson,D.G.				
TITLE	GROWTH FACTOR HOMOLOG ZVEGR4				
JOURNAL	Patent: JP 2002542825-A 2 17-DEC-2002;				
COMMENT	ZymoGenetics Inc				
OS	Artificial Sequence				
PN	JP 2002542825-A/2				
PD	17-DEC-2002				
PR	03-MAY-2000 JP 2000615760				
PR	03-MAY-1999 US 09/304216,10-NOV-1999 US 60/164463, PR				
PR	04-FEB-2000 US 60/180169				
PI	Paul o sheppard,charles e hart,teresa gilbert,debra g PI				
CC	degenerate sequence				
FT	Key Location/Qualifiers				
FT	misc_feature (1)..(1110)				
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ORIGIN					
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Best Local Similarity	100.0%; Pred. No. 2.8e-173;				
Matches 1109; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				

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DB 1 ATGCAYMGNYTNATHTYGTATATACNTTATHTSGCNAAYTTTGTGWSNTGWSNGAY 60

Qy	61	ACMNSNCNACNCCNCA RMSGCMWSNAHTHARCGNTTNMGNAAYGCNAAYTTNMGNGN	120
Db	61	ACMNSNCNACNCCNCA RMSGCMWSNAHTHARCGNTTNMGNAAYGCNAAYTTNMGNGN	120
Qy	121	GAYGARMSNAAYCAYYTNA CNGAYTNTATA VMGNNGNCA YGARPCNAHCA RGTNAARGN	180
Db	121	GAYGARMSNAAYCAYYTNA CNGAYTNTATA VMGNNGNCA YGARPCNAHCA RGTNAARGN	180
Qy	181	AAVGNTAYGTCNCA RMSNCCMNGTYY CCNAAYMSNTAYCCMGNAA YTTNTYNTNACN	240
Db	181	AAVGNTAYGTCNCA RMSNCCMNGTYY CCNAAYMSNTAYCCMGNAA YTTNTYNTNACN	240
Qy	241	TGGMGNTNCA VMSNCA RGARBAAYACMGNATTCAR TNGTNTTYTGA YAA YCAR TTYGGA	300
Db	241	TGGMGNTNCA VMSNCA RGARBAAYACMGNATTCAR TNGTNTTYTGA YAA YCAR TTYGGA	300
Qy	301	YTMGAR GARCNGARBAAYGAYATHGTG MGTAA GAYTTYTGNGAR GTCNGAR YATHMSN	360
Db	301	YTMGAR GARCNGARBAAYGAYATHGTG MGTAA GAYTTYTGNGAR GTCNGAR YATHMSN	360
Qy	361	GAAACMWSNA CNA THATHMNGMNGMTGGTYGNCAYAARGATNCCNMGNA TH	420
Db	361	GAAACMWSNA CNA THATHMNGMNGMTGGTYGNCAYAARGATNCCNMGNA TH	420
Qy	421	AA RSMNGNACNAAYCARATHAAR THACNTTAA RMSGAYAYATYTTGNTGNAR	480
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Qy	481	CCNGNTTYAARATHTTAYTAYMSNTYNTNGAR GAYTTYCAR CNGCNGCNGCNGMSNGAR	540
Db	481	CCNGNTTYAARATHTTAYTAYMSNTYNTNGAR GAYTTYCAR CNGCNGCNGCNGMSNGAR	540
Qy	541	ACNAAYTGGGARMSNTGNA CMMSMSNA THMSGSGCTMSNTAYAA VMSNCCMSNGTN	600
Db	541	ACNAAYTGGGARMSNTGNA CMMSMSNA THMSGSGCTMSNTAYAA VMSNCCMSNGTN	600
Qy	601	ACNGAYCCNA CYNTNATHG CNGAYGCNTYNGAYAAABAATHG CNGARTTYGAYACNGTN	660
Db	601	ACNGAYCCNA CYNTNATHG CNGAYGCNTYNGAYAAABAATHG CNGARTTYGAYACNGTN	660
Qy	661	GARGAYTNTYTAARATYTTTAYCCNGARMSNTGGCAR GAR GAYTTNGARBAAYTGTA Y	720
Db	661	GARGAYTNTYTAARATYTTTAYCCNGARMSNTGGCAR GAR GAYTTNGARBAAYTGTA Y	720
Qy	721	YTMGAYACNCCMNGTAYVMGNNGMNGMSNTAYCA YGAYMGAARMSNAARGTNCAAYTN	780
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Qy	781	GAYMGTNTNAAVGAYGVCNAAARMGNTAYMSNTGYACNCCMGNAA YTA VMSNCTNAY	840
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Qy	1021	MNGNGMNGCNAARACNAATGGCANTYNTGNGAYATHCAR YNTNGAYCA YCA GARGMGTGY	1080
Db	1021	MNGNGMNGCNAARACNAATGGCANTYNTGNGAYATHCAR YNTNGAYCA YCA GARGMGTGY	1080
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Db	1081	GAYTGATHTGYMSNMGNCCNCCNMG	1109

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TITLE Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/fallicoin
JOURNAL Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
MEDLINE 21092670
PUBMED 11162582
2 (bases 1 to 1428)
AUTHORS Hamada, T., Ue-Tel, K. and Miyata, Y.
JOURNAL Direct Submission
Submitted (25-OCT-1999) Teiyoshi Hamada, Nippon Medical School, Department of Pharmacology, 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan (E-mail: t-hamada@nms.ac.jp, Tel: 81-3-3822-2131 (ex. 5277), Fax: 81-3-5814-1684)
Location/Qualifiers

FEATURES
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1. 1428
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/cell_line="U373MG"
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gene
CDS

ORIGIN

Query Match 71.9%; Score 798; DB 9; Length 1428;
Best Local Similarity 56.4%; Pred. No. 2.9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

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61 ACNWSNCGACNCCNCAWSNCCNMSNATHAARGCNYTNMNAAYGCAAYTYNMNGN 120
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181 AAYGNTAYGTCNCAWSNCCNMGNTTCCNAAYSNNTAYCCNMGAAAYTYNTYTNACN 240
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577 AATATCAAGAGAACCAATTTAATATCACTTCAAGTCAGATGACTATCTTGTGGCTTAA 636
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Db 637 CCTGATTCAGATTTATTTATTTCTTGTGGAAGATTTCCAAACCCGACGACTTCAGAG 696
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LOCUS AX164744 1828 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent WO0125437.
ACCESSION AX164744
VERSION AX164744.1 GI:14545598
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Shinkets, R.A., Lichenstein, H., Hermann, J.L., Boldog, F.L.,
Minkoff, S. and Jeffers, M.
TITLE Growth factor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0125437-A 1 12-APR-2001;
Curegen Corporation (US)
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ORIGIN
Query Match 71.9%; Score 798; DB 6; Length 1828;
Best Local Similarity 56.4%; Pred. No. 2.9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
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Db 182 ATGACACCGGCTCATCTTGTGTCTACACTTAATCTGGGCAACTTTGGACGCTGGGAC 241
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LOCUS AX664403 1828 bp DNA linear PAT 24-MAR-2003
DEFINITION Sequence 3 from Patent WO02058716.
ACCESSION AX664403
VERSION AX664403.1 GI:29169373
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Jeffers, M., Shinkels, R.A., Prayaga, S., Boldog, F.L., Yang, M.,
Burgess, C.E., Fernandez, E.R., Riltman, B., Shinkels, J.B.,
Laroche, W.J., and Lichtenstein, H.S.
Treatment of inflammatory bowel disease using growth factors
Patent: WO 02058716-A3 01-AUG-2002;
Curagen Corporation (US)
FEATURES
Source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 71.9%; Score 798; DB 6; Length 1828;
Best Local Similarity 56.4%; Pred. No. 2,9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
QY 1 ATGCAVMTNTNATHHTYGTNTAYACNTYNTATHGNGNAAVYTYGWSNTGYMNGNAY 60
Db 182 ATGACACCGGCTCATCTTGTGTCTACACTTAATCTGGGCAACTTTGGACGCTGGGAC 241
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Db 1262 GATTGTATCTGACGTCAAGACCACTCG 1290

RESULT 7
AX704461 1828 bp DNA linear PAT 03-APR-2003
LOCUS AX704461
DEFINITION Sequence 1 from Patent WO02059618.
ACCESSION AX704461
VERSION AX704461.1 GI:29538585
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shinkoff, R.A., Lichenstein, H., Herrmann, J.L., Boldog, F.L.,
Minkoff, S., Jeffere, M., Andrews, D. and Larochele, W.
TITLE Growth factor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 02059618-A 1 01-AUG-2002;
Curegen Corporation (US)
FEATURES
source location/Qualifiers
1..1828
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Query Match 71.9%; Score 798; DB 6; Length 1828;
Best Local Similarity 56.4%; Pred. No. 2.9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

Qy 1 ATGCATMGNTYNTATHTTGTATVACNTNATHTGYGNAAYTTTGYMSNTGYMGAY 60
Db 182 ATGACCGGCTCATCTTGTCTCATCTATCTGCGCAACTTTTCAGCTGTGCGGAC 241
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RESULT 8
AF335584 1828 bp mRNA linear PRI 24-APR-2001
LOCUS AF335584
DEFINITION Homo sapiens platelet-derived growth factor D mRNA, complete cds.
ACCESSION AF335584

VERSION AF335584.1 GI:13774335
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1828)
AUTHORS Larochelle,W.J., Jeffere,M., McDonald,W.F., ChillaKur,R.A., Giese,N.A., Lokker,N.A., Sullivan,C., Boldog,F.L., Yang,M., Verne,C., Burgess,C.E., Fernandez,E., Deegler,L.L., Rittman,B., Shinkets,R.A., Rothenberg,J.M., and Lichenstein,H.S.
TITLE PDGF-D, a new platelet-activated growth factor
JOURNAL Nat. Cell Biol. 3 (5), 517-521 (2001)
MEDLINE 21231380
PUBMED 11331882
REFERENCE 2 (bases 1 to 1828)
AUTHORS Larochelle,W.J., Jeffere,M., Yang,M., Verne,C., Burgess,C.E., Fernandez,E., Shinkets,R.A., and Lichenstein,H.S.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Development, Curegen Corporation, 322 East Main Street, Branford, CT 06405, USA
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ORIGIN
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Beet Local Similarity 56.4%; Pred. No. 2.9e-173;
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DB 482 TTAGAGGAAGCAGAAATATATCTGTAGATGATTTGTAAGTTGAAGTAAATATCC 541
QY 361 GARACWSNACNATHTAHMNGNMGNTGTGVCNCAVARGATNCCNMGNAT 420

DB 542 GAAACCACTACATTTAGAGACGATGTGTGACAAAGAGTCTCTCAAGATA 601
QY 421 AARMSNMNACNAAYCARATHAARATHACNTTYAARMSNGAYATATTTGNCNAR 480
DB 602 AATTAAGAGAACCAATTAATTAATCAATTCAGATCGATCTTGTGTAA 661
QY 481 CCNGNTTYAARATHTATTAAYTNTNATNGARAGATTTTCARCCNGCNGCNGNNGAR 540
DB 662 CCGTATTCAGATTTATTTATTTCTTGTGTGAAGATTTCCAAACCGGACGAGCTTCAAG 721
QY 541 ACNAAVYTGARWSNNGINACNWSNMSNATHTWSNNGNMGNTNATYAAVWSNCCNWSN 600
DB 722 ACCAATCGGAATCTGTCAAGCTCTATTTCAAGGGGTATCTTCACTCTCAATCA 781
QY 601 ACNGAVCNACNNTNATHTGNCNAGVGCNTNCAVYARABARATHGNGARTTGAVACN 660
DB 782 ACGGATCCCTCATGATTTGGATGCGATCTGTGACAAAATTTGCAATTTGATCACTG 841
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DB 962 GATAGGCTCAATGAGAGCAAGGTTACAGTTGACATCCACAGAAATTTACTCGGTCAAT 1021
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DB 1022 ATAAGAGAGAGCTGAAGATTTGGCCAAATGTGCTTTTCAAGTGTGCTCTGTCAG 1081
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LOCUS Growth factor homolog zveg3.
DEFINITION
ACCESSION BD264400
VERSION BD264400.1 GI:33074168
KEYWORDS JP 2002531127-A/32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1882)
AUTHORS Gao,Z., Hart,C.B., Piddington,C.S., Sheppard,P.O., Shoemaker,K.E., Gilbertson,D.G., and West,J.W.
TITLE Growth factor homolog zveg3
JOURNAL Patent: JP 2002531127-A 32 24-SEP-2002;
ZYMOMETRICS INC
COMMENT OS Homo sapiens (human)
PN JP 2002531127-A/32
PD 24-SEP-2002
PF 07-DEC-1999 JP 2000586908
PR 07-DEC-1998 US 09/207120, 06-JUL-1999 US 60/142576 PR

21-OCT-1999 US 60/161653.12-NOV-1999 US 60/165255 PI ZEREN
GAO, CHARLES E HART, CHRISTOPHER S PIDDINGTON, PAUL O PI SHEPPARD,
PI KIMBERLY E SHOEMAKER, DEBRA G GILBERTSON, JAMES W WEST PC
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A61P35/00, A61P39/10, A61P39/14, A61P39/02, A61P27/06, A61P29/00, PC
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Query Match 71.9%; Score 798; DB 6; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAYMGNTYNTAHTTGTGNTAATGACATGCTTAATCTGGCGAACTTTGCGAGCTGCGGAGC 60
DB 226 ATGCACCGGCTCATCTTGTCTACACTTAATCTGGCGAACTTTGCGAGCTGCGGAGC 285
QY 61 ACNMSNGCNAACNCCNARMSNGCNSNATHTAARGCNYTMMGNAAYGCAAAAYTTMNGMNGN 120
DB 286 ACTTCTGCAACCCCGCAGAGCGATCATCAAGCTTTCGCAACCCCACTCAGGCGA 345
QY 121 GAYGARNNAAYCAAYTTNACGAYTTNTAYMGNGAGARACNATHTARNTNARGN 180
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DB 406 AAGGCTAGCTGAGAGTCTTGAATCCGAAACAGCTCCAGCAACCTGCTCTGACA 465
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RESULT 10
BD276211
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
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COMMENT
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PN JP 2002542825-A/1
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615760
PR 03-MAY-1999 US 09/304216, 10-NOV-1999 US 60/164463, PR
PI paul o sheppard, charles e hart, teresa gilbert, debra g pi
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FT CDS (226) . . (1338) .
source 1. 1882
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ORIGIN
Query Match 71.9%; Score 798; DB 6; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2.9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;

QY 1 ATGCAYMGNTYNTAHTTGTGNTAATGACATGCTTAATCTGGCGAACTTTGCGAGCTGCGGAGC 60
DB 226 ATGCACCGGCTCATCTTGTCTACACTTAATCTGGCGAACTTTGCGAGCTGCGGAGC 285
QY 61 ACNMSNGCNAACNCCNARMSNGCNSNATHTAARGCNYTMMGNAAYGCAAAAYTTMNGMNGN 120

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RESULT 11

AR238015
LOCUS AR238015 1882 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6468543.
ACCESSION AR238015
VERSION AR238015.1 GI:27282968
KEYWORDS
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REFERENCE
1 (bases 1 to 1882)
AUTHORS
TITLE
JOURNAL
FEATURES
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1. 1882
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ORIGIN
Query Match 71.9%; Score 798; DB 6; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2,9e-173; Indels 0; Gaps 0;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
Qy 1 ATGCAVMGNTYATHTYGTNTAYACNTYTNATHGTCGNAAYTYTYGYMSNTGYMNGAY 60
Db 226 ATGCAACGGCTCATCTTGTGTACACTGAATCTGCGAACTTTTGACAGCTGTGGGAC 285
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LOCUS Sequence 1 from patent US 6495668.
DEFINITION AR267253
ACCESSION AR267253.1 GI:29697256
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 1882)
AUTHORS Gilbert T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.
TITLE Growth factor homolog ZVEGF4
JOURNAL Patent: US 6495668-A 17-DEC-2002;
FEATURES
Location/Qualifiers
1. 1882
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Query Match 71.9%; Score 798; DB 6; Length 1882;
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Qy 1 ATGCAYMGNTYNAHTTGTNTAYACNTYNAHTTGYGNAAYTGTGWSNTGYWNGAY 60
Db 226 ATGCACCGGCTCATCTTGTCTTCACTCTTAATCTCGCAAACTTTTGCAGCTGTGCGGAC 285
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Db 1306 GATTGTATCTGCACCTCAAGACCACTCG 1334

RESULT 13
AR282980 1882 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 36 from patent US 6528050.
DEFINITION AR282980
ACCESSION AR282980
VERSION AR282980.1 GI:29719801
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1882)
AUTHORS Gao, Z., Hart, C.E., Piddington, C.S., Sheppard, P.O., Shoemaker, K.E.,
TITLE Gilbertson, D.G., and West, J.W.
JOURNAL Growth factor homolog zvegf3
Patent: US 6528050-A 36-04-MAR-2003;
FEATURES
Location/Qualifiers
1. 1882
Source /organism="unknown"

Db 766 ACCAAGTGGAGTCTGTCAAGAGCTCTATTTCAGGGGATCTCTAATCTCCATCTCA 825
Qy 601 ACNGAYCCNAACNTTAATGCGNAYGNTYNGAARARATHGNGARTTYGAYACGNTN 660
Db 826 ACGATTCGCTCAAGTACTTCAATCCAGATGCAATGCAAGAAAGATCTTGAAATATGAT 945
Qy 661 GARGAYTNTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
Db 886 GAGATCTGCTCAAGTACTTCAATCCAGATGCAATGCAAGAAAGATCTTGAAATATGAT 945
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Qy 841 ATHTNGAGARAYTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 1066 ATAGAGAGAGAGTGAAGTTGGCCATGCTGCTCTTCCAGCTTCCCTCTCTGCTGAG 1125
Qy 901 MGNTRYGNGGNAATYTGNGNTYNGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAY 960
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Qy 961 GGNARAACNGTNAARATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
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Db 1246 AGGGATGAGCTTAAGACATGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1305
Qy 1081 GAYTGAATHTGYMSNMNGNCCNMG 1109
Db 1306 GATTGATCTGAGCTCAAGACCACTCTG 1334
RESULT 15
AX044487 1882 bp DNA linear PAT 24-NOV-2000
LOCUS AX044487
DEFINITION Sequence 1 from Patent WO066736.
ACCESSION AX044487
VERSION AX044487.1 GI:11343345
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.
TITLE Growth factor homolog zveg4
JOURNAL Patent: WO 066736-A 1 09-NOV-2000;
ZymoGenetics, Inc. (US)
FEATURES
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1. 1882
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226. 1338
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226. 1338
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PGFKIYSLDEPQAASETNMEVSISGVSPSTYDITDILADLADKRIAEFD
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Query Match 71.9%; Score 798; DB 6; Length 1882;
Best Local Similarity 56.4%; Pred. No. 2,9e-173;
Matches 626; Conservative 300; Mismatches 183; Indels 0; Gaps 0;
Qy 1 ATGCAVMGNTYNTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
Db 226 ATGCAACCGGCTCATCTTGTCTACACTCTAATCTGCGAACTTTGACGCTGCGGAC 285
Qy 61 ACNNGNCAACNCCNCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db 286 ACTTCTGACACCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345
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Qy 181 AAYGNTAYGTCNCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
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Qy 241 TGGMNTYNTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300
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Qy 301 YTNAGARAGCNGARAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
Db 526 TTAGAGGAGAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 585
Qy 361 GARGAASNAACNATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
Db 586 GAACACGATCACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 645
Qy 421 AARSNGNACNAAYCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Db 646 AATCAAGAGAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 705
Qy 481 CNGGNTYNTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Db 706 CTTGATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 765
Qy 541 ACNAAATYGGARWSNGTNAACNMSNATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Db 766 ACCAAGCTGGGAATCTGTCAAGAGCTATTTCAAGGGGTATCTTAATCACTCTCATAGTA 825
Qy 601 ACNAGAYCCNATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Db 826 ACGATTCGCTCAAGTACTTCAATCCAGATGCAATGCAAGAAAGATCTTGAAATATGAT 945
Qy 721 YTNAGAYCCNAGNTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Db 946 CTGAGACCCCTCGATTCGAGGAGGATCATACATGACCGAAGTCAAAAAGTTGACCTG 1005
Qy 781 GAYGNTYNAAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAY 840
Db 1006 GATAGGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065
Qy 841 ATHTNGAGARAYTNAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 1066 ATAGAGAGAGAGTGAAGTTGGCCATGCTGCTCTTCCAGCTTCCCTCTGCTGAG 1125
Qy 901 MGNTRYGNGGNAATYTGNGNTYNGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAY 960
Db 1126 CGCTGTGAGAGAAATTTGCTGTGAGAACTGCAATGAGAGGCTCCGACATGCAATGCA 1185
Qy 961 GGNARAACNGTNAARATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Db 1186 GGGAAAACCGTGAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1245

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Result No.	Score	Query Match	Length	DB	ID	Description
1	261.6	72.1	1095	9	AY419997	AY419997 Homo sapi
2	261.6	72.1	1095	9	AY419998	AY419998 Pan trogl
3	261.6	72.1	3739	3	AF113216	AF113216 Homo sapi
4	244	67.2	455	7	CO600294	CO600294 D68-1c24
5	244	67.2	533	7	CO658472	CO658472 D634-2023
6	244	67.2	1095	9	AY419999	AY419999 Mus muscu
7	244	67.2	1797	3	AK003359	AK003359 Mus muscu
8	243	66.9	551	7	CO596606	CO596606 D68-13011
9	242.4	66.8	532	7	CO611691	CO611691 D59-107b5
10	240.8	66.3	554	7	CO603983	CO603983 D68-274a2
11	239.8	66.1	533	7	CO632657	CO632657 D69-116a1
12	198.8	56.8	813	5	E0335658	E0335658 603514418
13	190.4	52.5	579	5	BU407817	BU407817 603483546
14	189.4	52.2	735	6	CD100521	CD100521 AGENCOUR
15	186.2	51.3	855	6	CD362407	CD362407 AGENCOUR
16	174.2	48.0	560	2	AW666905	AW666905 EST380981
17	168.6	46.4	774	5	BU290871	BU290871 603607229
18	166.4	45.8	819	5	E0335805	E0335805 603477657
19	145.8	40.2	761	7	CN078301	CN078301 EC2BBA141
20	144.8	39.9	360	1	AA488780	AA488780 aa54c10..r
21	137.2	37.8	811	5	BU326859	BU326859 603489244
22	137	37.7	966	6	CD242494	CD242494 AGENCOUR
23	133.4	36.7	798	5	BU404150	BU404150 603482511
24	131.8	36.3	727	5	BU326159	BU326159 603493550

25	121	33.3	985	5	BUI11960	603405533
26	120.6	33.2	723	4	B1689894	603010727
27	111.8	30.8	2993	3	BC029699	B0188984
28	110.2	30.4	411	6	CB802513	603031903
29	110.2	30.4	423	6	CB802513	603031903
30	110.2	30.4	523	3	BF021379	AGNCNDC:S
31	110.2	30.4	712	4	B1693338	BF021679
32	110.2	30.4	823	5	BUI614825	UY50105.Y
33	110.2	30.4	901	5	B0957838	603043666
34	110.2	30.4	1038	9	AY403295	603043666
35	110.2	30.4	2765	3	AK052947	AGNCNDC:S
36	110.2	30.4	3244	3	AK033734	UY50105.Y
37	110.2	30.4	3455	4	AK042767	603043666
38	110	30.3	546	4	BG609411	603043666
39	109.6	30.2	559	4	BM053596	603043666
40	108.8	30.0	610	7	CN308276	603043666
41	108.8	30.0	769	6	CB309471	603043666
42	108.8	30.0	802	4	B1870535	603043666
43	108.8	30.0	1038	9	AY403293	603043666
44	108.8	30.0	1142	4	BG681390	603043666
45	108.8	30.0	2655	3	BC051876	603043666

ALIGNMENTS

RESULT 1

AY419997

DEFINITION

ACCEPTATION

ACCESSION
VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

REFERENCE AUTHORS

evolution

1

TITLE

FORMAT

JOURNAL
DITMED

REFERENCE

REFERENCE AUTHORS

ESTR 7

TITLE
JOURNAL

JOURNAL

COMMENT

1

FEATURES

SOURCE

gene

1

ORIGIN

—

Query Mail Post 1.00

Best Local Matches

Maldives

QY

1

D5

LOCUS	CO658472/c	533 bp	mRNA	linear	EST 23-JUL-2002
DEFINITION	CO658472				
Db	121	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	180		
Qy	121	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	180		
Db	264	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	205		
Qy	181	ACGCTGTAATGTCGAGGCTGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	240		
Db	204	ACGCTGTAATGTCGAGGCTGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	240		
Qy	241	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	300		
Db	144	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	85		
Qy	301	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	360		
Db	84	GTGCTGTTTCTTCCCGGCTGCTGCTGAGGCGCTGTGAGGTAAGTGGCTGTGGA	25		
Qy	361	MG 362			
Db	24	CG 23			

RESULT 5				
LOCUS	CO658472/c			
DEFINITION	DG34-2023 DG34-uterus Camts familiaris CDNA 3', mRNA sequence.	533 bp	linear	EST 23-JUL-2002
ACCESSION	CO658472			
VERSION	CO658472.1	GI:50575262		
KEYWORDS	EST.			

SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE	1 (bases 1 to 533)
AUTHORS	Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H., Heinrich,J., and Loebebert,R.
TITLE	Dog arrayTAG cDNA clone collection
JOURNAL	unpublished (2004)
COMMENT	Contact: Thomas Schlueter LION Bioscience AG Walldorferstrasse 98, D-69123 Heidelberg, Germany Tel.: +49 6221 4038 150 Fax: +49 6221 4038 290 Email:Thomas.Schlueter@lionbioscience.com.

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FEATURES
SOURCE
    Email: Thomas.Schluter@ionbioscience.com.
    location/Qualifiers
    1..533
    /organism="Canis familiaris"
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Query Match      67.2%  Score 244;  DB 7;  Length 533;
Query Local Similarity 53.6%  Pred. No. 4.1e-56;
Matches 194;  Conservative 97;  Mismatches 71;  Indels 0;  Gaps 0
ORIGIN
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/clone_id="DG34-uterus"
/note="Organ: uterus; Vector: Dog pBluescript LION"

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•

Db 401 TCCATCAGCATGACAGAAAGGTCAAAAGGTGAGCCTGAGCCGGCTCAATGTAAGATGTCAAAGGC 342
 Oy 61 TAYMNTGYACNCCMGNAAATYAWNSNTNAAATYTHMGNGARGARYTAARTYTNCGNAA 120
 Db 341 TATAGCTGACATCCTTAGGAAATTACTCGGTCAACTAAGAGAGAGCTAGAAGTGACCCAC 282
 Oy 121 GTNGTNTTYYTCCMAGNTGYTYNTYNTGNTCAABMGNTGGGNGAAATGYGAGNTGYGAGN 180
 Db 281 GTGGCTCTCTTCCCGCTGGCTCTCTCTGACAGCGCTGTGAGGTAACCTGTGGCTGTGGA 222

Db	Query Match	Best Local Similarity	Matches	Score	244	DB	9	Length	1095
Db	221	ACCATCATCTGGAATCTCTTACTGACATCTGGGAAAACTGTAAAAAATATCTATG	162						
Qy	241	GTNYTNCARTTYGARCCNGNCAYATHAPARMNMNGNMGNACNAPACNATGACNYTN	300						
Db	161	GTATTGAAAGTTTGAGCCTGCGCATTTTCAAGAGAGGGGAGACGAGCAAGCATNGSTCTT	102						
Qy	301	GTNGAVATHCARTYNAGCYACYGARMENTGTGATGTATHTGTGYSNMNMNCNCN	360						
Db	101	GTTCACATCCAGCTGGATCCATGACGAGCGGTGTGATTTGATCTGTAGCTCCGACCACT	42						
Qy	361	MG 362							
Db	41	CG 40							
RESULT 6									
LOCUS	AY419999	1095 bp	DNA	linear	GSS 12-DEC-2000				
DEFINITION	Mus musculus HCM7077 gene, VIRtual TRANSCRIPT, partial sequence,								
ACCESSION	AY419999								
VERSION	AY419999.1	GI:39775956							
KEYWORDS	GSS.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
AUTHORS	1 (bases 1 to 1095) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.								
TITLE	Interferring nonneutral evolution from human-chimp-mouse orthologous gene trios								
JOURNAL	Science 302 (5652), 1960-1963 (2003)								
PUBMED	14671302								
REFERENCE	2 (bases 1 to 1095)								
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.								
TITLE	Direct Submission								
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA								
COMMENT	This sequence is made by sequencing genomic exons and ordering them based on alignment.								
FEATURES	Location/Qualifiers								
SOURCE	1..1095								
gene	/organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>1095 /locus_tag="HCM7077"								
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Query Match	67.2%	Score 244	DB 9	Length 1095					
Best Local Similarity	53.6%	Pred. No. 6,2e-56							
Matches 194	Conservative	97	Mismatches 71	Indels 0	Gaps 0				
Qy	1	MSNTATCAAGYAGMGAARMSNARNGATGAYTTNGAYNGYNTNAAYGAYGACNAARMGN	60						
Db	730	TCATATACATATATTCGAAAGTCCAAAGTACCTGACAGAGCTCATATGATGATCAAGCGT	789						
Qy	61	TAYVSTNGYACNCCNMGNAAYTAYWSNGTNAAYATHMGNAARGARYTNARNTNGCAAT	120						
Db	790	TACAGTTGCACTCCACAGATCTCTGTGAACCTCAGAGAGAGAGCTGAAGCTGACCAAT	849						
Qy	121	GTNGTNTTNTTTCNNMNTGYTNTYNTGTNCARMGNTGYGANGGNAAYTGYGNTGYGN	180						
Db	850	GCAGTCTTCTTCCACAGATGCTCTCGTGCAGGCGTGTGTGGCAACTGTGTTGCGA	909						
Qy	181	ACNGTNAAYTGGMGMSNTGYACNTGTAAATWSNGGNAARACNGTNAARATATYCAAYGAR	240						

[illegible]

208 A C C A T T C A A C T T G G A A A C T T T A A A A A T A T C A T G A G 149

[illegible]

[illegible]

LOCUS	BUJ39658	813 bp	MRNA	linear	EST 28-NOV-2002
DEFINITION	605514148P1 CSEBCHN66	Gallus gallus	cDNA	clone	CHEST451d5 5', mRNA sequence.
ACCESSION	BUJ39658				
VERSION	BUJ39658.1	GI:25847659			
KEYWORDS	EST.				
SOURCE	Gallus gallus (chicken)				
ORGANISM	Gallus gallus				
REFERENCE	Eukaryota; Neutroa; Chordata; Craniota; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
AUTHORS	1 (bases 1 to 813) Boardman, P.E., Sans-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.				
TITLE	A Comprehensive Collection of Chicken CDNAS				
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)				
MEDLINE	22335534				
PUBMED	12445392				
COMMENT	Contract: Simon Hubbard Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 10D, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk.				
FEATURES	Location/Qualifiers				
source	1..813 /organism="Gallus gallus" /mol_type="mRNA" /strain="White Leghorn, Hisex" /db_xref="taxon:9031" /clone="CHEST451d5" /dev_stage="16 day embryo" /lab_host="DH10B" /clone_lib="CSEBCHN66" /note="Organ: brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntend, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adopted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."				
ORIGIN					
Query Match	54.8%;	Score 198.8;	DB 5;	Length 813;	
Best Local Similarity	48.8%;	Pred. No. 1.6e-43;			
Matches 180;	Conservative 92;	Mismatches 89;	Indels 8;	Gaps 1;	
1	WSNTAYCAVGYMGNNAARWSNAARCTGAYTTNGATYMGNTYNAAYGAYGCAAAAGN 60				
440	AGCTACATGACAGAGAAAGTCCAAAGTGTGACCTGCAGCAGCTGAATGATGTGAAGGC 499				
61	TAYWSNTGYACNCCNMGNAAYTAYWSNGTNAAYVTHMGNGARGARYTNAARYTNGCNA 120				
500	TACAGCTGCACTCCAGAAACTACTCTGTCAATTTAAGGGAAGAACTGAGCTGACAAAT 559				
121	GTNCTNTTYYTTCGMMNTGYTNTYNTGTCNABKNGTGYGNGGNAAYVGTGNTGNGN 180				
560	GCTGTTTTCTTCCTCGCTGCTCTCTTGTCCAGGCGCTGTGAGAAATTTGTGCTGTGA 619				
181	ACNGTNAAYTGGMGMSNTGYAANTGYAAVYWSNGNNAARACNGTNAARATATCAVAG 240				
620	ACTTCAATATNGAAATCTCTGACGTGATGTCCGGGAAACAGTGAATAATATCATGAG 679				
241	GTNTYNTCAATTGAGRC-----NGNCAYATTAARMGNTGNGMGNCNAARACNA 292				

Db	680	CTGTGTAATTTTGTCCCGAGGGGAGCATCCCGAAGAAGCAAGCAAGCAAGCA	739
Qy	293	TGGCTNTGTNGAYATHCARYTNGAYCAVCAGARMGNTGYATGTATHTGYMSNM	352
Db	740	TGCTTATGATGATATACAGTTGATCATCATCATGATGCTGTGATTCATCTGCA	799
Qy	353	GNCNCNCNM 361	
Db	800	GACCAGCCC 808	
RESULT 13	BU407817	579 bp	mRNA
LOCUS	603483546F1	CSROCHN59	Gallus gallus
DEFINITION	sequence.		clone CHEST374112 5', mRNA
ACCESSION	BU407817		
VERSION	BU407817.1	GI:25776873	
KEYWORDS	EST.		
SOURCE	Gallus gallus (chicken)		
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
AUTHORS	1 (bases 1 to 579)		
TITLE	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,		
JOURNAL	Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.		
MEDLINE	A Comprehensive Collection of Chicken cDNAs		
PUBMED	Curr. Biol. 12 (22), 1965-1969 (2002)		
COMMENT	12445392		
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	/lab_host="DH10B"		
	/clone_id="CSROCHN59"		
	/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was bluntended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."		
ORIGIN			
Query Match	53.5%;	Score 190.4;	DB 5;
Best Local Similarity	49.7%;	Prod. No. 2.8e-41;	
Matches 184;	Conservative 91;	Mismatches 85;	Indels 10;
		Gaps 2;	
Qy	1	WSNTAYCAYGAYGCMARFMSNARGTNGAYTTGAYGMYNTNAYGAYGCMNARCMGN	60
Db	205	AGCTACCATGACAGGAAGTCCAAAGTTGACCTCGAAGCGCTGAATATGATGTGACGC	264

[illegible]

FEATURES	Source
LOCUS	CD100521
DEFINITION	AGENCOURT_13996064 NICHD_XGC_Tad1 Xenopus laevis cDNA clone
ACCESSION	IMAGE:6940282 5', mRNA sequence.
VERSION	CD100521
KEYWORDS	CD100521.1 GI:30750648
SOURCE	EST.
ORGANISM	Xenopus laevis (African clawed frog)
REFERENCE	Xenopus laevis
AUTHORS	Bukacinska, Wietasza; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus. 1 (bases 1 to 735)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Drs. Donald Brown and Liqun Cai cDNA Library Preparation: CLONTECH cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LNCM3266 row: h column: 09 High quality sequence stop: 587.
FEATURES	Location/Qualifiers
Source	1..735
	/organism="Xenopus laevis"
	/mol_type="mRNA"
	/db_xref="taxon:8355"
	/clone="IMAGE:6940282"
	/dev_stage="metamorphosis stage 53"
	/clone_lib="NICHD_XGC_Tad1"
	/note="Organ: Developing Tadpole; Vector: pDNR-LIB; Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGAGCGCGCCGACAG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.6 kb (range 0.9-3.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match	52.2%	Score 189.4;	DB 6;	Length 735;
Best Local Similarity	47.7%	Pred. No. 6.1e-41;		
Matches 177; Conservative	90;	Mismatches 95;	Indels 9;	Gaps 1

QY	1	MSNTAAYCAAYGAMGAANAAMSNARBTNGAYYTNGAYMGNYTNAAGAYACGCNAAIRMGN	60
Db	56	ACATTTCAGAABAAAATAATCGAABAATCAATTGGACAAGACTTAATGATGATCTCAAGCC	115
QY	61	TAYWSNTGYACNCNMGNAAAYTAYWSNGTNAAYATHMENGARGARYTNAARYTNGMAAY	120
Db	116	TACAGCTGTACTCCAAGAAATTAACACAGTAATTTAAAGAAAGAAATTTAAAAATTAACAAT	175
QY	121	GTNGINTTTYTYCCMGMNTGYTYNTTNGTNCARMENITGYGNGMAAYTYGYGNTGYGN	180
Db	176	GCTGATATCTTCTTCGATGCCCTGCTCATCAAGCCCTGGGAGGAAACGTGCTGCCGA	235
QY	181	ACNGTNAAYTGGMGMNSNTGYACNTGYAAVMSNGNABARA.CNGTNAARAARTAYCAYGAR	240
Db	236	ACACCAAACGTGGAATCTTGTATTTGTACAGCTGGCAAAACGTGAAAAAATACCATGAG	295
QY	241	GTNYTNCARTTYGARCCNG-----GNCAVATHAARMGNMGNNGNCNAA.RACN	291
Db	296	GTGCTGAAAGTCATGCCCCGAAAAACA.GTAA.CAACAAAAA.ACGAAG.CCAAT.TCCAAGAT	355
QY	292	ATGGCNTYNGTNGA.VATHCAR.TYNGAY.CAYCAYGAR.MGNTGY.GATGY.THTHGYS.NB.N	351
Db	356	ATGTCAT.TYTGGA.CAT.CCA.GCTTAG.CAYCAT.GAGCGA.YTGAT.TGTAT.TT.CG.CAG.TTCT	415
QY	352	MGNCCNCCNMG	362
Db	416	AGGCCCACTCG	426

RESULT 15					
CD362407					
LOCUS					
DEFINITION	CD362407	855 bp	mRNA	linear	EST 29-MAY-2001
	AGENCOURT_14239070	NICHD_XC_Bnl	Xenopus	laevis	cDNA clone
	IMAGE:6956855	5',	mRNA sequence.		

ACCESSION	CD362407
VERSION	CD362407.1
KEYWORDS	EST.
SOURCE	Xenopus laevis (African clawed frog)
ORGANISM	Xenopus laevis

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (baaes 1 to 855)	NIH-MGC	http://mgc.ncl.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Daniela S. Gerhard, Ph.D.			

National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaphis-remail.nih.gov
 Tissue Procurement:
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL4584 row: J column: 22
 High quality sequence stop: 723.

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FEATURES      location/Qualifiers
SOURCE        1. .855
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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6956855"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"

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/clone_1fb="NICHD_Xgc Brn1"
 name="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection
 (XGC) library."

Query Match	Similarity	51.3%	Score 186.2	DB 6	Length 855
Best Local	Similarity	47.2%	Pred. No. 5.1e-40		
Matches	175	Conservative	90	Mismatches	97
				Indels	9
				Gaps	1
Qy	1	WSNTAYCAYGAYMGNAARMSNAARGTNGAYYTNAGYMGNTYNAAYGAYGAYCNAARPMGN	60		
Db	146	ACITTTTCAGAAAAAATACTCAAAGTCAATTTGACAGGCTTAATGATGATGCAAGCAC	205		
Qy	61	TAYMSNTGYACNCCMGAAATAYMSNTNAAYATHMGNGARGARYTAAAYTNGCNAAY	120		
Db	206	TACAGCTGTACTCCAGAGAAATTACACGTGAATTTAAGAGAAGAAATTAATAATTACAAAT	265		
Qy	121	GTNGTNTTYYTCCNMGNTGYTYTYNTYNTGNCARMGNTGYGGNGNAAYTGYGNTGYGN	180		
Db	266	GCTGTATTCCTTCCTCGATGCTGCTGTACTCAAGGGCTGTGAGAGAACTGGGGCTGGCGG	325		
Qy	181	ACNGTNAAYTGMGWSNTGYACNTGYAAYTMSNGNAAACNGTNAAPAAATAYATYAR	240		
Db	326	ACACCGAAGCTGGAAATCTTGTGTTGTACATCTGTGGCAAAACAGTGAATAAATACCATAG	385		
Qy	241	GTNTYTCARTTYGAACGCG-----GNCAYATHAARMGNGMGWNGCNAARACN	291		
Db	386	GTGCTGAAGAGTAATGCCGAGAAAACAGTATCAACAAAAAACAAAGAGCAATCCAGAAAT	445		
Qy	292	ATGCGNTYNTGNAAYATHCARNTNGAYCAYCAYARGMGNTGYGATGYATHTGSWMSN	351		
Db	446	ATGTCAATTGTGACATTCACGCTTGAGCATCACGAGCGATGTGATGTATCTGCAGTCT	505		
Qy	352	MGNCCNCCMG 362			
Db	506	AGGCDACCTCG 516			

Search completed: November 15, 2004, 20:15:27
Job time : 1927.65 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 18:05:02 ; Search time 1055.48 Seconds
(without alignments)
1857.496 Million cell updates/sec

Title: US-09-876-813-6_COPY_748_1110

Perfect score: 363
Sequence: 1 wantacaycagymgnarw.....gyenwanmgnccnccmgn 363

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubna/US11_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261.6	72.1	369	US-10-403-142-41	Sequence 41, App
2	261.6	72.1	620	US-10-276-774-717	Sequence 717, App
3	261.6	72.1	881	US-10-365-095-32	Sequence 32, App
4	261.6	72.1	1041	US-10-403-142-45	Sequence 45, App
5	261.6	72.1	1110	US-09-876-813-6	Sequence 6, App
6	261.6	72.1	1162	US-10-028-072-185	Sequence 185, App
7	261.6	72.1	1162	US-10-140-808-185	Sequence 185, App
8	261.6	72.1	1162	US-10-121-049-185	Sequence 185, App
9	261.6	72.1	1162	US-10-123-904-185	Sequence 185, App
10	261.6	72.1	1162	US-10-140-470-185	Sequence 185, App
11	261.6	72.1	1162	US-10-175-746-185	Sequence 185, App
12	261.6	72.1	1162	US-10-176-918-185	Sequence 185, App

13	261.6	72.1	1162	US-10-176-921-185	Sequence 185, App
14	261.6	72.1	1162	US-10-137-865-185	Sequence 185, App
15	261.6	72.1	1162	US-10-140-474-185	Sequence 185, App
16	261.6	72.1	1162	US-10-142-431-185	Sequence 185, App
17	261.6	72.1	1162	US-10-143-114-185	Sequence 185, App
18	261.6	72.1	1162	US-10-140-002-185	Sequence 185, App
19	261.6	72.1	1162	US-10-142-419-185	Sequence 185, App
20	261.6	72.1	1162	US-10-123-262-185	Sequence 185, App
21	261.6	72.1	1162	US-10-142-423-185	Sequence 185, App
22	261.6	72.1	1162	US-10-121-050-185	Sequence 185, App
23	261.6	72.1	1162	US-10-141-755-185	Sequence 185, App
24	261.6	72.1	1162	US-10-143-032-185	Sequence 185, App
25	261.6	72.1	1162	US-10-123-108-185	Sequence 185, App
26	261.6	72.1	1162	US-10-123-236-185	Sequence 185, App
27	261.6	72.1	1162	US-10-123-261-185	Sequence 185, App
28	261.6	72.1	1162	US-10-140-821-185	Sequence 185, App
29	261.6	72.1	1162	US-10-140-828-185	Sequence 185, App
30	261.6	72.1	1162	US-10-121-045-185	Sequence 185, App
31	261.6	72.1	1162	US-10-123-292-185	Sequence 185, App
32	261.6	72.1	1162	US-10-123-903-185	Sequence 185, App
33	261.6	72.1	1162	US-10-124-819-185	Sequence 185, App
34	261.6	72.1	1162	US-10-124-822-185	Sequence 185, App
35	261.6	72.1	1162	US-10-140-825-185	Sequence 185, App
36	261.6	72.1	1162	US-10-160-498-185	Sequence 185, App
37	261.6	72.1	1162	US-10-124-824-185	Sequence 185, App
38	261.6	72.1	1162	US-10-127-825A-185	Sequence 185, App
39	261.6	72.1	1162	US-10-127-829A-185	Sequence 185, App
40	261.6	72.1	1162	US-10-127-835A-185	Sequence 185, App
41	261.6	72.1	1162	US-10-127-839A-185	Sequence 185, App
42	261.6	72.1	1162	US-10-127-901A-185	Sequence 185, App
43	261.6	72.1	1162	US-10-128-693A-185	Sequence 185, App
44	261.6	72.1	1162	US-10-131-813A-185	Sequence 185, App
45	261.6	72.1	1162	US-10-131-818A-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-10-403-142-41
; Sequence 41, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD;
; FILE REFERENCE: 21402-573A
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 09/64286
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/688598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/694159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: CursSeqList version 0.1
; SEQ ID NO 41
; LENGTH: 369

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(369)
US-10-403-142-41

Query Match 72.1%; Score 261.6; DB 17; Length 369;
Best Local Similarity 56.6%; Pred. No. 9.6e-66; Indels 0; Gaps 0;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WNTATYCAAYGAMGNAARMSNAARGTNGAYTTNGAYMGNTYNAAYGAYGCGNAARMGN 60
DB 7 TCATACCATGACCGGAAGTCAGAAAGTTGACCTGGATAGGCTCAATGATGTCACAGCCT 66
QY 61 TAAWNTGYACNCCMGNNAAYTAYWNGTNAAYATHMGNGAGARTNAARTTNGCNAAY 120
DB 67 TACAGTTGCACTCCCGAGAAATTACTGGTCAATTAAGAGAAAGAGCTGAAGTTGGCCAT 126
QY 121 GINGNTTYYTTCNNMNTGYTYNTNGTNCARMGNTGYGNGGNAAYTYGGANTGYGNG 180
DB 127 GTGGCTCTCTTCCAGCTTGCCCTCCTCGTGACGCGCTGTGAGGAAATTGTGGCTGTGA 186
QY 181 ACNGTNAAYTGAGMWSNTGYACNTGYAAYWNSGNAARAACGTNAARAARTAYCAAGAR 240
DB 187 ACTGTCACTGGAGGCTCTGCAACATGCAATTCAGGGAACCGTGAAAAAGTATCATGAG 246
QY 241 GNTYTCARTTYGARCNGNCAAYATHAARMGNGMNGGNAARAACNAATGGCANTN 300
DB 247 GTATTACAGTTTGAGCTGCGCCACATCAAGAGAGGGGATGAGCTTAAGCCATGCTCTTA 306
QY 301 GINGAYATHCARNTNGAYCAAYGARMGNTGYAYTYGATHGYWNSMNGMNCNCN 360
DB 307 GTTGACATCCAGTTGATGATCAATGAAACGATGTGATGATCTGACGCTCAAGACCACT 366
QY 361 MG 362
DB 367 CG 368

RESULT 2
US-10-276-774-717
Sequence 717, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 717
LENGTH: 620
TYPE: DNA
ORGANISM: Homo sapiens
US-10-276-774-717

Query Match 72.1%; Score 261.6; DB 16; Length 620;
Best Local Similarity 56.6%; Pred. No. 1.4e-65; Indels 0; Gaps 0;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WNTATYCAAYGAMGNAARMSNAARGTNGAYTTNGAYMGNTYNAAYGAYGCGNAARMGN 60
DB 96 TCATACCATGACCGGAAGTCAGAAAGTTGACCTGGATAGGCTCAATGATGTCACAGCCT 155
QY 61 TAAWNTGYACNCCMGNNAAYTAYWNSGNTYAAAYATHMGNGAGARTNAARTTNGCNAAY 120

DB 156 TACAGTTGCACTCCCGAAGTAATTACTGGCTCAATATAAGAGAAAGCTGAAGTTGGCCAT 215
QY 121 GINGNTTYYTTCNNMNTGYTYNTNGTNCARMGNTGYGNGGNAAYTYGGANTGYGNG 180
DB 216 GTGGCTCTCTTCCAGCTTGCCCTCCTGTGCAAGGCTGTGAGGAAATTTGGGCTGTGA 275
QY 181 ACNGTNAAYTGAGMWSNTGYACNTGYAAYWNSGNAARAACGTNAARAARTAYCAAGAR 240
DB 276 ACTGTCACTGGAGGCTCTGCAACATGCAATTCAGGGAACCGTGAAAAAGTATCATGAG 335
QY 241 GNTYTCARTTYGARCNGNCAAYATHAARMGNGMNGGNAARAACNAATGGCANTN 300
DB 336 GTATTACAGTTTGAGCTTGGCCACATCAAGAGAGGGGTGAGCTTAAGACCATGGCTCTA 395
QY 301 GINGAYATHCARNTNGAYCAAYGARMGNTGYAYTYGATHGYWNSMNGMNCNCN 360
DB 396 GTTGACATCCAGTTGATGATCAATGAAACGATGTGATGATCTGACGCTCAAGACCACT 455
QY 361 MG 362
DB 456 CG 457

RESULT 3
US-10-365-095-32
Sequence 32, Application US/10365095
Publication No. US20030224488A1
GENERAL INFORMATION:
APPLICANT: Fox, Brian A.
APPLICANT: Moore, Margaret D.
APPLICANT: Swiderex, Kristine M.
FILE REFERENCE: 01-33
TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
CURRENT APPLICATION NUMBER: US/10/365,095
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 60/355,882
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 881
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pTAP339 insert
US-10-365-095-32

Query Match 72.1%; Score 261.6; DB 15; Length 881;
Best Local Similarity 56.6%; Pred. No. 1.8e-65; Indels 0; Gaps 0;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WNTATYCAAYGAMGNAARMSNAARGTNGAYTTNGAYMGNTYNAAYGAYGCGNAARMGN 60
DB 105 TCATACCATGACCGGAAGTCAGAAAGTTGACCTGGATAGGCTCAATGATGTCACAGCCT 164
QY 61 TAAWNTGYACNCCMGNNAAYTAYWNSGNTYAAAYATHMGNGAGARTNAARTTNGCNAAY 120
DB 165 TACAGTTGCACTCCCGAAGTAATTACTGGCTCAATTAAGAGAAAGCTGAAGCTGACAT 224
QY 121 GINGNTTYYTTCNNMNTGYTYNTNGTNCARMGNTGYGNGGNAAYTYGGANTGYGNG 180
DB 225 GTGGCTCTCTTCCAGCTTGCCCTCCTCGTGACGCGCTGTGAGGAAATTGGGCTGTGA 284
QY 181 ACNGTNAAYTGAGMWSNTGYACNTGYAAYWNSGNAARAACGTNAARAARTAYCAAGAR 240
DB 285 ACTGTCACTGGAGGCTCTGCAACATGCAATTCAGGGAACCGTGAAAAAGTATCATGAG 344
QY 241 GNTYTCARTTYGARCNGNCAAYATHAARMGNGMNGGNAARAACNAATGGCANTN 300
DB 345 GTATTACAGTTTGAGCTTGGCCACATCAAGAGAGGGGTGAGCTTAAGACCATGGCTCTA 404
QY 301 GINGAYATHCARNTNGAYCAAYGARMGNTGYAYTYGATHGYWNSMNGMNCNCN 360

DB 405 GTTGACATCCAGTTGGATCACCATGACGATGATGATCTGCGACGCTCAAGACCACT 464
QY 361 MG 362
DB 465 CG 466

RESULT 4

US-10-403-142-45
; Sequence 45, Application US/10403142
; Publication No. US20040162236A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573A
; CURRENT APPLICATION NUMBER: US/10/403,142
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 08/969106
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/369065
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/604286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/651200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/662783
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/686598
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 09/694159
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/918779
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/964956
; PRIOR FILING DATE: 2001-09-26
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: Curoseqblast version 0.1
; SEQ ID NO 45
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1041)
US-10-403-142-45

Query Match 72.1%; Score 261.6; DB 17; Length 1041;
Best Local Similarity 56.6%; Pred. No. 2.1e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 MSNTAYCAYGAYMGNAARNSNARGTNGAYYTNNGAYMGNTNAAAYGAYGAYGCNAAABGN 60
DB 679 TCATACCAATGAGCTGGAAGTGAAGCTGAGTCAATTAAGAGAGAGTCCAAAGCGT 738
QY 61 TAYMSNTGYACNCNMGNAAATAYWSNGTNAAYATHMNGARGARYTNAARYTNCNAY 120
DB 739 TACAGTTCACCTCCAGGAATTAACGGTCAATTAAGAGAGAGTGAAGTGGCCAT 798
QY 121 GTNGNTTYYTTCMGNNTGYTNTNGTNCARMGNTGYGNGNAAATGYGNTGYGN 180
DB 739 GTGGCTCTTTCACAGCTGCTCCTCGTGCAGCCCTGTGGAAGAAATGTGCTGTGA 858
QY 181 ACNGTNAAYTGGMGMSNTGYACNTGYAAYWSNGNABARACNGTNAARARATAYCAYGAR 240
DB 859 ACTGTCAACTGAGGCTCTGTCATGATGATCAAGGAAACCGTGAAGAAAGATATCATGAG 918
QY 241 GTNTYTCARTTYGACCCGNGNCAYATHAARMGNMGNGMNGCNAARACNATGSCNTYN 300
DB 919 GTATTACAGTTTGAAGCTGCGCACATCAAGAGAGGGGTAGAGCTTAAGACATGCTCTTA 978

QY 301 GTNGAYATHCARNTNGAYCAYCAYGARBMNTGYATGYATHGTYSWMSNMGCNCN 360
DB 979 GTTGACATCCAGTTGGATCACCATGACGATGATGATCTGCGACGCTCAAGACCACT 1038
QY 361 MG 362
DB 1039 CG 1040

RESULT 5

US-09-876-813-6
; Sequence 6, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc_feature
; LOCATION: (1)..(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-813-6

Query Match 72.1%; Score 261.6; DB 11; Length 1110;
Best Local Similarity 100.0%; Pred. No. 2.2e-65;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNTAYCAYGAYMGNAARNSNARGTNGAYYTNNGAYMGNTNAAAYGAYGAYGCNAAABGN 60
DB 748 MSNTAYCAYGAYMGNAARNSNARGTNGAYYTNNGAYMGNTNAAAYGAYGAYGCNAAABGN 807
QY 61 TAYMSNTGYACNCNMGNAAATAYWSNGTNAAYATHMNGARGARYTNAARYTNCNAY 120
DB 808 TAYMSNTGYACNCNMGNAAATAYWSNGTNAAYATHMNGARGARYTNAARYTNCNAY 867
QY 121 GTNGNTTYYTTCMGNNTGYTNTNGTNCARMGNTGYGNGNAAATGYGNTGYGN 180
DB 868 GTNGNTTYYTTCMGNNTGYTNTNGTNCARMGNTGYGNGNAAATGYGNTGYGN 927
QY 181 ACNGTNAAYTGGMGMSNTGYACNTGYAAYWSNGNABARACNGTNAARARATAYCAYGAR 240
DB 928 ACNGTNAAYTGGMGMSNTGYACNTGYAAYWSNGNABARACNGTNAARARATAYCAYGAR 987
QY 241 GTNTYTCARTTYGACCCGNGNCAYATHAARMGNMGNGMNGCNAARACNATGSCNTYN 300
DB 988 GTNTYTCARTTYGACCCGNGNCAYATHAARMGNMGNGMNGCNAARACNATGSCNTYN 1047
QY 301 GTNGAYATHCARNTNGAYCAYCAYGARBMNTGYATGYATHGTYSWMSNMGCNCN 360
DB 1048 GTNGAYATHCARNTNGAYCAYCAYGARBMNTGYATGYATHGTYSWMSNMGCNCN 1107
QY 361 MG 362

Db 1108 MG 1109

RESULT 6
US-10-028-072-185
Sequence 185, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550

PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29

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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 19/98-06-11
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match      72.1%  Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

Qy 1 WSNATYCAVGYMGNAAARWNSNARGTNGAYTYTNGAYMGNNTYNAAYGAYGVCNNAARMGN 60
Db 761 TCATRCACATGACCGGAAGTCAAAAGTTGACCTGATAGGCTCAATGATGATGCCAAGGT 820
Qy 61 TAYWSNTGYACNCCMGNAAATYATWSNGTNAAYATHTMNGARGARYTNAARYTNGCNAY 120
Db 821 TACAGTTGCATCCCGAGAAATTAATCTCGATATATAGAGAAAGAGCTGAAGTTGCCAAT 880
Qy 821 TACAGTTGCATCCCGAGAAATTAATCTCGATATATAGAGAAAGAGCTGAAGTTGCCAAT 880
```

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Qy 121 GTNGTNTYTTYCCNMNGTGYTYNTNGTNCARMGNTGYGNGNAAATGYGNTGYGN 180
Db 881 GTGGCTCTTTCACAGCTTGCTCCTCGTGCAGGCTGTGAGAGAAATTTGGCTGTGA 940
Qy 181 ACGNTNAAVTGGMGNWSTGYACNTGYAATWSNGNNAARACNGTNAARAAATYATYCAR 240
Db 941 ACTGCATCTGAGAGCTCTGCACATGCAATTCAGGAAACCGGAAATAATCATATAG 1000
Qy 241 GTNTNCAATTYGARCNGNCAVATTAABRMGNNGMNGMNGCNAAACNATGCGNVTN 300
Db 1001 GTATTACGTTTGAGCTCGGCAATTCAGAGAGGGGTAAAGCTTAAGACCATGCTTTA 1060
Qy 301 GTNGAYATHCARYTNGAYCAVCAVARGMNTGYATGYATHTGYWSNWSMNGCNCCN 360
Db 1061 GTTGACATCCAGTTGATGATCAATGAAGATGCGATTGTATCTGACGCTCAAGCACCT 1120
Qy 361 MG 362
Db 1121 CG 1122

RESULT 7
US-10-140-808-185
; Sequence 185, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 185
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-808-185

Query Match      72.1%  Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

Qy 1 WSNATYCAVGYMGNAAARWNSNARGTNGAYTYTNGAYMGNNTYNAAYGAYGVCNNAARMGN 60
Db 761 TCATRCACATGACCGGAAGTCAAAAGTTGACCTGATAGGCTCAATGATGATGCCAAGGT 820
Qy 61 TAYWSNTGYACNCCMGNAAATYATWSNGTNAAYATHTMNGARGARYTNAARYTNGCNAY 120
Db 821 TACAGTTGCATCCCGAGAAATTAATCTCGATATATAGAGAAAGAGCTGAAGTTGCCAAT 880
Qy 121 GTNGTNTYTTYCCNMNGTGYTYNTNGTNCARMGNTGYGNGNAAATGYGNTGYGN 180
Db 881 GTGGCTCTTTCACAGCTTGCTCCTCGTGCAGGCTGTGAGAGAAATTTGGCTGTGA 940
Qy 181 ACGNTNAAVTGGMGNWSTGYACNTGYAATWSNGNNAARACNGTNAARAAATYATYCAR 240
Db 181 ACGNTNAAVTGGMGNWSTGYACNTGYAATWSNGNNAARACNGTNAARAAATYATYCAR 240
```

```
Db 941 ACTGTCACTGAGAGTCTGTCGACATGCAATTCAGGGGAAAACCGTGAAGAAAGTATCATGTAG 1000
Qy 241 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Db 1001 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Qy 301 GTTGAATATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Db 1061 GTTGAATATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1120
Qy 361 MG 362
Db 1121 CG 1122
```

RESULT 8

```
US-10-121-049-185
; Sequence 185, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C17
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION: US/10/121,049
; NUMBER OF SEQ ID NOS: 550
; SEQUENCE OF SEQ ID NOS: 550
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-185
```

```
Query Match 72.1%; Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;
```

```
Qy 1 WSNATAYCAGAYMGNAAARWNAARGTNGAYYTNAGAYMGNATYNAAYGAYGCAAAAMGN 60
Db 761 TCATACATGACGCGAGATGCAAAAGTTGACCTGATGCTCAATGATGATGCCAACCGT 820
Qy 61 TAYMSNTGYACNCCMGNAAATYATWSNGTNAAYATHTMGNGARGARYYTNAARYTNGCNAAY 120
Db 821 TACAGTTGACCTCCAGGAATTAATCTCGTCAATATTAAGAGAGAGCTGAGAGTTGGCCAAAT 880
Qy 121 GTNGTNTTYTTCNMGNTGYTNTYTNGTNCABMNTGYGNGGNAAYTGTGNTGYGN 180
Db 881 GTGCTCTTCTTCCACGTTGCTCTCTGTCGACGCTGTGAGGAAATTTGTGCTGTGGA 940
Qy 181 ACGTNAAYTGGMWSNTGYACNTGYAAYWSNGNAAACNGTNAARAARTAYCAAGAR 240
Db 941 ACTGTCACTGAGAGTCTGTCGACATGCAATTCAGGAGAAACCGTGAAGAAAGTATCATGTAG 1000
Qy 241 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Db 1061 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1120
```

```
Db 1001 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Qy 301 GTTGAATATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Db 1061 GTTGAATATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1120
Qy 361 MG 362
Db 1121 CG 1122
```

RESULT 9

```
US-10-123-904-185
; Sequence 185, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C54
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION: US/10/123,904
; NUMBER OF SEQ ID NOS: 550
; SEQUENCE OF SEQ ID NOS: 550
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-185
```

```
Query Match 72.1%; Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;
```

```
Qy 1 WSNATAYCAGAYMGNAAARWNAARGTNGAYYTNAGAYMGNATYNAAYGAYGCAAAAMGN 60
Db 761 TCATACATGACGCGAGATGCAAAAGTTGACCTGATGCTCAATGATGATGCCAACCGT 820
Qy 61 TAYMSNTGYACNCCMGNAAATYATWSNGTNAAYATHTMGNGARGARYYTNAARYTNGCNAAY 120
Db 821 TACAGTTGACCTCCAGGAATTAATCTCGTCAATATTAAGAGAGAGCTGAGAGTTGGCCAAAT 880
Qy 121 GTNGTNTTYTTCNMGNTGYTNTYTNGTNCABMNTGYGNGGNAAYTGTGNTGYGN 180
Db 881 GTGCTCTTCTTCCACGTTGCTCTCTGTCGACGCTGTGAGGAAATTTGTGCTGTGGA 940
Qy 181 ACGTNAAYTGGMWSNTGYACNTGYAAYWSNGNAAACNGTNAARAARTAYCAAGAR 240
Db 941 ACTGTCACTGAGAGTCTGTCGACATGCAATTCAGGAGAAACCGTGAAGAAAGTATCATGTAG 1000
Qy 241 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Db 1001 GTTATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Qy 301 GTTGAATATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1060
Db 1061 GTTGAATATTCACATGTTGAGCTGGCCGACATCAAGAGAGGGGTAGACCAATGAGGCTCTTA 1120
```

Oy 361 MG 362
Db 1121 CG 1122

RESULT 10

US-10-140-470-185
; Sequence 185, Application US/10140470
; Publication No. US2003002231A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 185
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-185

Query Match 72.1%; Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

Oy 1 WSNATYCAVGYMGNAAAFWSNAAAGTNGAYTNGAYMGNNTNAAVYGAAYGACNAARMGN 60
Db 761 TCATACACATGACCGGAAGTCAAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGCGT 820
Oy 61 TAYNSNGYACNCCMGNAAATAYVNSNGTNAAYATHMNGARGARYTNAAYTNGCNAY 120
Db 821 TACAGTTGACCTCCAGAGAAATTAATCGGTCAATATAAGAGAAAGCTGAAGTTGGCCAT 880
Oy 121 GTNGNTTYYTTCNMGNTGYTNTNGTNCARBMNGTGYGNGNAAVYGYGNTGYGN 180
Db 881 GTGGCTTCTTCCACGTTGCTCTCTCGTGCAGCGCTGTGAGAGAAATTTGGCTGTGGA 940
Oy 881 GTGGCTTCTTCCACGTTGCTCTCTCGTGCAGCGCTGTGAGAGAAATTTGGCTGTGGA 940
Db 941 ACTGCACTGAGAGGCTGCGACATGCAATTCAGGAGAAACCGTGAATAAAGTATCATAG 1000
Oy 181 ACNGTNAAYTGGMWSNTGYACNTGYAAYVNSNGNAAACNGTNAADPAARTAYCAVGR 240
Db 241 GTNTNCAATYTGACCGNCAVATHAARMNGMNGMNGCNAAACNAATGCGCNTN 300
Oy 241 GTNTNCAATYTGACCGNCAVATHAARMNGMNGMNGCNAAACNAATGCGCNTN 300
Db 1001 GTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGGCTCTTA 1060
Oy 301 GTNGAYATHCARVYNGAYCAVYAGARMGNTGYATHTGYVNSWMSMNGCNCCN 360
Db 1061 GTTGACATCCAGTTGATACCATGACATGACATGACATGATCTGTGACGCTCAAGACCACT 1120
Oy 361 MG 362
Db 1121 CG 1122

RESULT 11

US-10-175-746-185
; Sequence 185, Application US/10175746
; Publication No. US20030027270A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 185
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-746-185

Query Match 72.1%; Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

Oy 1 WSNATYCAVGYMGNAAAFWSNAAAGTNGAYTNGAYMGNNTNAAVYGAAYGACNAARMGN 60
Db 761 TCATACACATGACCGGAAGTCAAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGCGT 820
Oy 61 TAYNSNGYACNCCMGNAAATAYVNSNGTNAAYATHMNGARGARYTNAAYTNGCNAY 120
Db 821 TACAGTTGACCTCCAGAGAAATTAATCGGTCAATATAAGAGAAAGCTGAAGTTGGCCAT 880
Oy 121 GTNGNTTYYTTCNMGNTGYTNTNGTNCARBMNGTGYGNGNAAVYGYGNTGYGN 180
Db 881 GTGGCTTCTTCCACGTTGCTCTCTCGTGCAGCGCTGTGAGAGAAATTTGGCTGTGGA 940
Oy 881 GTGGCTTCTTCCACGTTGCTCTCTCGTGCAGCGCTGTGAGAGAAATTTGGCTGTGGA 940
Db 941 ACTGCACTGAGAGGCTGCGACATGCAATTCAGGAGAAACCGTGAATAAAGTATCATAG 1000
Oy 181 ACNGTNAAYTGGMWSNTGYACNTGYAAYVNSNGNAAACNGTNAADPAARTAYCAVGR 240
Db 241 GTNTNCAATYTGACCGNCAVATHAARMNGMNGMNGCNAAACNAATGCGCNTN 300
Oy 241 GTNTNCAATYTGACCGNCAVATHAARMNGMNGMNGCNAAACNAATGCGCNTN 300
Db 1001 GTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTAGAGCTTAAGACCATGGCTCTTA 1060
Oy 301 GTNGAYATHCARVYNGAYCAVYAGARMGNTGYATHTGYVNSWMSMNGCNCCN 360
Db 1061 GTTGACATCCAGTTGATACCATGACATGACATGACATGATCTGTGACGCTCAAGACCACT 1120
Oy 361 MG 362
Db 1121 CG 1122

RESULT 12
US-10-176-918-185
; Sequence 185, Application US/10176918
; Publication No. US20030027275A1

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/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P330R1C382
/ CURRENT APPLICATION NUMBER: US/10/176,918
/ PRIORITY FILING DATE: 2002-06-20
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 185
/ LENGTH: 1162
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-176-918-185
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Query Match 72.1%; Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;
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QY 1 WSNATYCAVAGYAGMNAARMSNARGTNGAYVYTNMGAYVYTNAAVYAGVAGCNAAARMGN 60
DB 761 TCATACCATGACCGGAAGTCAGAAAGTTGACCTGATGAGCTCATATGATGATGCAAGCGT 820
QY 61 TAYWSNTGYACNCCNMGNAAYTAVWSNGTNAAYATMNGARGARYTNAARYTNGCNAY 120
DB 821 TACAGTTGACCTCCAGAGAAATTACTCGCTCATATTAAGAGAAAGCTGAAGTTGGCCAT 880
QY 121 GTNGTNTTYTTCNMGNTGYTNTYNTGNCARMGNTGYGNGNAAVYGGNTGYGN 180
DB 881 GTGGCTTCTTCCACGTTGCTCTCTCGTGCAGCGCTGTGAGGAAATTGGCTGTGGA 940
QY 181 ACNGTNAAYTGAGMWSNTGYACNTGYAAYWSNGNNAARACNGTNAARAPATAYCAGAR 240
DB 941 ACTGCACTGAGAGCTCTGCACTGCAATTCAGGAAACCCTGAAAGATATCATGAG 1000
QY 241 GTNYTCARTTYGARCNGCNGCAVATHAARMGNGMNGNNGNNAARACNATGGCNYTN 300
DB 1001 GTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTGAGCTTAAGACATGCTCTA 1060
QY 301 GTNGAYATHCARNTNGAYCAVYAGVAGMNTGYATGYATHTGYWSMNGNCCNCCN 360
DB 1061 GTTGACATCACTTGATGATCAACATGAAGATGCGATTGTATCTGCACTCAAGACCACT 1120
QY 361 MG 362
DB 1121 CG 1122
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RESULT 13
US-10-176-921-185
/ Sequence 185, Application US/10176921
/ Publication No. US20030027276A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
```

```
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P330R1C288
/ CURRENT APPLICATION NUMBER: US/10/176,921
/ PRIORITY FILING DATE: 2002-06-20
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 185
/ LENGTH: 1162
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-176-921-185
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Query Match 72.1%; Score 261.6; DB 14; Length 1162;
Best Local Similarity 56.6%; Pred. No. 2.3e-65;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;
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QY 1 WSNATYCAVAGYAGMNAARMSNARGTNGAYVYTNMGAYVYTNAAVYAGVAGCNAAARMGN 60
DB 761 TCATACCATGACCGGAAGTCAGAAAGTTGACCTGATGAGCTCATATGATGATGCAAGCGT 820
QY 61 TAYWSNTGYACNCCNMGNAAYTAVWSNGTNAAYATMNGARGARYTNAARYTNGCNAY 120
DB 821 TACAGTTGACCTCCAGAGAAATTACTCGCTCATATTAAGAGAAAGCTGAAGTTGGCCAT 880
QY 121 GTNGTNTTYTTCNMGNTGYTNTYNTGNCARMGNTGYGNGNAAVYGGNTGYGN 180
DB 881 GTGGCTTCTTCCACGTTGCTCTCTCGTGCAGCGCTGTGAGGAAATTGGCTGTGGA 940
QY 181 ACNGTNAAYTGAGMWSNTGYACNTGYAAYWSNGNNAARACNGTNAARAPATAYCAGAR 240
DB 941 ACTGCACTGAGAGCTCTGCACTGCAATTCAGGAAACCCTGAAAGATATCATGAG 1000
QY 241 GTNYTCARTTYGARCNGCNGCAVATHAARMGNGMNGNNGNNAARACNATGGCNYTN 300
DB 1001 GTATTACAGTTTGAGCTGGCCACATCAAGAGAGGGGTGAGCTTAAGACATGCTCTA 1060
QY 301 GTNGAYATHCARNTNGAYCAVYAGVAGMNTGYATGYATHTGYWSMNGNCCNCCN 360
DB 1061 GTTGACATCACTTGATGATCAACATGAAGATGCGATTGTATCTGCACTCAAGACCACT 1120
QY 361 MG 362
DB 1121 CG 1122
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RESULT 14
US-10-137-865-185
/ Sequence 185, Application US/10137865
/ Publication No. US20030032155A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
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OM nucleic - nucleic search, using sw model

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(without alignments)
5510.484 Million cell updates/sec

Title: US-09-876-813-6_Copy_748_1110

Perfect score: 363

Sequence: 1 wsnrtaycaygagymgnarws.....gywnwsmgncncncmgn 363

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261.6	72.1	1110	US-09-564-595D-6	Sequence 6, Appl1
2	261.6	72.1	1162	US-10-140-002-185	Sequence 185, App
3	261.6	72.1	1882	US-09-457-066-36	Sequence 36, Appl
4	261.6	72.1	1882	US-09-540-224-1	Sequence 1, Appl1
5	261.6	72.1	1882	US-09-564-595D-1	Sequence 36, Appl
6	261.6	72.1	1882	US-09-706-968-36	Sequence 36, Appl
7	261.6	72.1	1882	US-09-808-972-1	Sequence 1, Appl1
8	261.6	72.1	1934	US-09-438-046-5	Sequence 5, Appl1
9	261.6	72.1	2253	US-09-438-046-7	Sequence 3, Appl1
10	254.4	70.1	690	US-09-438-046-3	Sequence 3, Appl1
11	244	67.2	1472	US-09-540-224-3	Sequence 3, Appl1
12	244	67.2	1472	US-09-564-595D-52	Sequence 52, Appl
13	244	67.2	1472	US-09-808-972-3	Sequence 3, Appl1
14	144.8	33.9	360	US-09-438-046-1	Sequence 1, Appl1
15	110.8	30.5	1035	US-09-457-066-6	Sequence 6, Appl1
16	110.8	30.5	1035	US-09-706-968-6	Sequence 6, Appl1
17	110.8	30.4	3571	US-09-457-066-42	Sequence 42, Appl
18	110.2	30.4	3571	US-09-564-595D-34	Sequence 34, Appl
19	110.2	30.4	3571	US-09-706-968-42	Sequence 42, Appl
20	110.2	30.4	3571	US-09-823-033-3	Sequence 3, Appl1
21	108.8	30.0	1035	US-09-468-647-3	Sequence 3, Appl1
22	108.8	30.0	1095	US-09-457-066-50	Sequence 50, Appl
23	108.8	30.0	1095	US-09-706-968-50	Sequence 50, Appl
24	108.8	30.0	1760	US-09-457-066-1	Sequence 1, Appl1
25	108.8	30.0	1760	US-09-564-595D-32	Sequence 32, Appl
26	108.8	30.0	1760	US-09-706-968-1	Sequence 1, Appl1
27	108.8	30.0	1760	US-09-823-033-1	Sequence 1, Appl1

28	108.8	30.0	2825	3	US-09-040-220D-1	Sequence 1, Appl1
29	108.8	30.0	2825	4	US-09-265-686-1	Sequence 1, Appl1
30	108.8	30.0	2825	4	US-09-723-749-1	Sequence 1, Appl1
31	108.8	30.0	2849	4	US-10-140-002-285	Sequence 285, App
32	46	12.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
33	45.6	12.6	832	4	US-09-621-976-2813	Sequence 2813, Ap
34	44.4	12.2	1141	4	US-09-806-7088-22	Sequence 8976, Ap
35	43.8	12.1	399	4	US-09-621-976-8976	Sequence 14, Appl
36	43.8	12.1	7218	1	US-08-232-463-14	Sequence 15639, A
37	43.2	11.9	505	4	US-09-621-976-15639	Sequence 15639, A
38	42.6	11.7	474	4	US-09-621-976-18033	Sequence 18033, A
39	41.4	11.4	1141	4	US-09-806-7088-22	Sequence 22, Appl
40	40.8	11.2	364	4	US-09-621-976-17202	Sequence 17202, A
41	40.4	11.1	364	4	US-09-621-976-17202	Sequence 17202, A
42	40.2	11.1	505	4	US-09-621-976-15639	Sequence 15639, A
43	39.2	10.8	1055	4	US-09-806-7088-23	Sequence 23, Appl
44	38.6	10.6	289	3	US-09-007-005-17	Sequence 17, Appl
45	38.6	10.6	289	3	US-09-244-796-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-09-564-595D-6
; Sequence 6, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564, 595D
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304, 216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc feature
; LOCATION: (1)..(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-564-595D-6

Query Match          72.1%; Score 261.6; DB 4; Length 1110;
Best Local Similarity 100.0%; Pred. No. 3e-71;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WSNRTAYCAYGAYMGNAARWNSNARAGTNGAYTNGAYMGNTNAAAYGAYGACNAARMGN 60
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DB      748 WSNRTAYCAYGAYMGNAARWNSNARAGTNGAYTNGAYMGNTNAAAYGAYGACNAARMGN 807

QY      61 TAYMSNTGYACNCCMGNAATAYTAYMSNCTNAAAYTTHMGNGARGARYTMAAYTNGCNAY 120
        |||||||
DB      808 TAYMSNTGYACNCCMGNAATAYTAYMSNCTNAAAYTTHMGNGARGARYTMAAYTNGCNAY 867

QY      121 GTNGNTTYYTTCNMGNTGYTYTYTNGTNCARMGNTGYGNGGNAAYTGYGNTGYGNG 180
        |||||||
DB      868 GTNGNTTYYTTCNMGNTGYTYTYTNGTNCARMGNTGYGNGGNAAYTGYGNTGYGNG 927

QY      181 ACNGTNAAYTGGMGNSNTGYACNTGYAAYVNSGNGNARACNGTNAARPAATAYCAVGAR 240
        |||||||
DB      928 ACNGTNAAYTGGMGNSNTGYACNTGYAAYVNSGNGNARACNGTNAARPAATAYCAVGAR 987
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QY	241	GTNYNRCARTTYGAACCGNGNCACVATTHAABRMNMGNMGNMGCAAAACNAATGCANTN	300
Db	988	GTYNTMCARTTYGARCNCNGNCAYATHAABRMNMGNMGNMGCAAAAPCNAATGGCNTN	1047
QY	301	GTNAPAYHCAARNTNGAICAYCARBARGNTGYGATYGATHTGTYSWMSNMGCCNCCN	360
Db	1048	GTNGATTAHCAKYTNMGATCAICAGARMGNTGYGATYGATHTGTYSWMSNMGCCNCCN	1107
QY	361	MG 362	
Db	1108	MG 1109	

RESULT 2

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/ Sequence 185, Application US/10140002
/ US-10-140-002-185
/
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: DeNovoys, Inc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Geo, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C59
/ CURRENT APPLICATION NUMBER: US/10/140,002
/ CURRENT FILING DATE: 2002-05-06
/ Prior Application removed - See Palm or File Wrapper
/ NUMBER OF SEQ ID NOS: 550
/ SFO ID NO 185
/ LENGTH: 1162
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-140-002-185

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Query Match	72.1%	Score 261.6	DB 4	Length 1162
Best Local Similarity	56.6%	Pred. No. 3.2e-71		
Matches	205	Conservative	97	Mismatches 60; Indels 0; Gaps 0;
QY	1	WSNTYCAVGAYMGAARMSNARAGTNGAYVYNGAYVMGYNTAAAGAYGAYCAACBAKGN	60	
Db	761	TCATCCCACTGACCGGAAGCTCAAAAGTTGACCTCGGATAGAGCTCAAGAAGATGCCAAGGT	820	
QY	61	TAYSNITGYACNCCNMENAAATYVSNGTNAAATATMNGARGARYTAARTNGCNAY	120	
Db	821	TACAGTSCACTCCCAAGAAATTACTCGGTCAATATAAGAGAAGCTAAAGTTGCCAAT	880	
QY	121	GTNGTNTTYYTCCMNGTGYTNTYNTGNCARMGNTGYGNGNAAATGYGANTGYG	180	
Db	881	GTGGCTTCTTCCACGTTGGCTCTCTCGTGAAGCGCTGTGAGGAAATTGGCTGTGGA	940	
QY	181	ACNGTNAAYTGGMGMWSNTGYAONTGVAAVMSNGNANARCNGTNAAAPAAATYCAVGAR	240	
Db	941	ACTGTCAACTGAAGGTCTCTGCACATGCAATTCAGGAAAAACGTGAAMAAAGTATCATGAG	1000	
QY	241	GTNTYNCARTTYGARCCNGNCACAYATHAARMGNMNGNMGNGNANARACNATGGCVNTN	300	
Db	1001	GTATTACAGTTTGAGCTCGTGGCCATCATCAAGAGGAGGGGTAGAGCTTAAGACCATAGCTCTTA	1060	

QY 301 GTGACATTCAR.YTNGA.VCA.VCA.VGARMGNTG.VA.YTTHG.TGYSNM.SMGNCNCN 360
 Db 1061 GTTCACATCCAGTTGCATCA.CCACTGAACGATGCATGTATCTGCAGCTCAAGCACCT 1120
 QY 361 MG 362
 Db 1121 CG 1122

RESULT 3

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US-09-457-066-36
; Sequence 36, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZYGF33
; FILE REFERENCE: 99-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (226)...(1338)
; US-09-457-066-36

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Query Match	72.1%	Score 261.6	DB 4	Length 1882
Best Local Similarity	56.6%	Pred. No. 4.7e-71		
Matches 205; Conservative	97;	Mismatches 60;	Indels 0;	Gaps 0

QY		MSNTAYCAGYGYMGNMARMSMAAAGTNGAYTTNGACVMTGNTNAAVGAIVGAYGCNAARWEN	60
Dd	973	TCATPACCATGACCGGAAAGTCAAAAATTGACTGTGATGGCTCAATGATGATGCCAAGCGT	10320
QY	61	TAYWSNTGYACNCNCNMNNAAYTAIYWSNGTNAAAYATHMGNGARGARYNTNAAAYTNGCNAA	120
Dd	1033	TACAGTTGCACTCCACAGGAATTACTCGGTCAATTAAGAAGAGCTGMACTTGCCAAIT	10920
QY	121	GTMCTNTTTTTYYCCMMNTGYTYNYTNGINCARMGNTGYGGNGNAAVTVYGNTGYGN	180
Dd	1093	GTGGTCTCTCTTCCACGTTGCCCTCTCTGTGCAGCGCTGTGGAGGAAATTTGGCTGTGGA	11520
QY	181	ACNGTNAAYVYGMGNMWSNTGYACNTGYAAVWSNGNABARCNGTNNABAARTYACAAGR	240
Dd	1153	ACGTCAACTGGAGAGTCTCTGCAATGCAATTCAGAGGAAAACTGTAAAAAGATCATGAG	1212
QY	241	GMYTNCARTTTYGARCCNGNCAVYTHAAPMGNGMNGNNGCNAARACNATGGCNYTN	300
Dd	1213	GATATTAAGATTTAGCTGCTGCCAACATCAAGAGAGGGGTGAGACTAAGACCATGGCTTA	1272
QY	301	GTNGAVYATHCARLYTNAGYCAVCAVGARMGNTGYATGVYTHGYNSMNSMNGCNCN	360
Dd	1273	GTTGACATCCAGTTGATGATCACCATGAACGATGGATGTATTCGTGACCTCAAGACCACT	1332
QY	361	MG 362	
Dd	1333	CG 1334	

RESULT 4

US-09-540-224-1
; Sequence 1, Application US/09540224
; Patent No. 6468543

Query Match 72.1%; Score 261.6; DB 4; Length 1882;

Best Local Similarity 56.6%; Pred. No. 4.7e-71;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

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QY 1 WSNATACAYAGVAMGNARMSNARGTNGAYTNGAYMGNVYTNAAVGAAYGCNAARMGN 60
Db 973 TCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGT 1032
QY 61 TAYMSNTGYACNCCNMGNAAYTAYMSNGTNAAYATMGNGARGARTNARATNCNAY 120
Db 1033 TACAGTTGACCTCCCGAAGATTTCTCGTCAATATTAAGAAAGAGCTGAAGTTGGCCAT 1092
QY 121 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1152
Db 1093 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1152
QY 181 ACNGTNAAYTGMGNMSTNGVACNTGYAAYMSNGNAARACNGTNAARARATYCAVGR 240
Db 1153 ACTGTCAACTGAGAGGCTCTGTCACATGCAATTCAGAGGAAACCGTGAAAAAGTATCATGAG 1212
QY 241 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1212
Db 1213 GTATTACAGTTTGAGCTTGGCCATCAAGAGAGGGGTAGAGCTTAAGATCATGCTCTTA 1272
QY 301 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1272
Db 1273 GTTGCATTCAGTTGAGTGCATCAATCAAGAGAGGGGTAGAGCTTAAGATCATGCTCTTA 1332
QY 361 MG 362
Db 1333 CG 1334
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RESULT 7
US-09-808-972-1

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/ Sequence 1, Application US/09808972
/ Patent No. 6630142
/ GENERAL INFORMATION:
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Topouzis, Stavros
/ APPLICANT: Gilbertson, Debra G.
/ TITLE OF INVENTION: METHOD OF TREATING FIBROPROLIFERATIVE
/ FILE REFERENCE: 00-79
/ CURRENT APPLICATION NUMBER: US/09/808,972
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: US 60/235,295
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/564,595
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/132,250
/ PRIOR FILING DATE: 1999-05-03
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 1882
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (226)...(1338)
US-09-808-972-1
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Query Match 72.1%; Score 261.6; DB 4; Length 1882;
Best Local Similarity 56.6%; Pred. No. 4.7e-71;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

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QY 1 WSNATACAYAGVAMGNARMSNARGTNGAYTNGAYMGNVYTNAAVGAAYGCNAARMGN 60
Db 973 TCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGT 1032
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QY 61 TAYMSNTGYACNCCNMGNAAYTAYMSNGTNAAYATMGNGARGARTNARATYNGCNAAY 120

Db 1033 TACAGTTGACCTCCCGAAGATTTCTCGTCAATATTAAGAAAGAGCTGAAGTTGGCCAT 1092

QY 121 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1152

Db 1093 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1152

QY 181 ACNGTNAAYTGMGNMSTNGVACNTGYAAYMSNGNAARACNGTNAARARATYCAVGR 240

Db 1153 ACTGTCAACTGAGAGGCTCTGTCACATGCAATTCAGAGGAAACCGTGAAAAAGTATCATGAG 1212

QY 241 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1212

Db 1213 GTATTACAGTTTGAGCTTGGCCATCAAGAGAGGGGTAGAGCTTAAGATCATGCTCTTA 1272

QY 301 GTCGTCCTCTTCCAGGTTGCTCCCTCGTGCAGCGCTGTGAGGAATGTGGCTGTGA 1272

Db 1273 GTTGCATTCAGTTGAGTGCATCAATCAAGAGAGGGGTAGAGCTTAAGATCATGCTCTTA 1332

QY 361 MG 362

Db 1333 CG 1334

RESULT 8
US-09-438-046-5

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/ Sequence 5, Application US/09438046
/ Patent No. 6706687
/ GENERAL INFORMATION:
/ APPLICANT: ERIKSSON, Ulf
/ APPLICANT: AASE, Karin
/ APPLICANT: LEE, Xuri
/ APPLICANT: PONTN, Annica
/ APPLICANT: TUTELA, Marko
/ APPLICANT: ALITALO, Kari
/ APPLICANT: OESTMAN, Arne
/ APPLICANT: HELDIN, Carl-Henrik
/ TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
/ FILE REFERENCE: Ulf Eriksson et al 1064-44833
/ CURRENT APPLICATION NUMBER: US/09/438,046
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: 60/107,852
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: 60/113,997
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/150,604
/ PRIOR FILING DATE: 1999-08-26
/ PRIOR APPLICATION NUMBER: 60/157,108
/ PRIOR FILING DATE: 1999-10-04
/ PRIOR APPLICATION NUMBER: 60/157,756
/ PRIOR FILING DATE: 1999-10-05
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 1934
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(966)
US-09-438-046-5
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Query Match 72.1%; Score 261.6; DB 4; Length 1934;
Best Local Similarity 56.6%; Pred. No. 4.8e-71;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

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QY 1 WSNATACAYAGVAMGNARMSNARGTNGAYTNGAYMGNVYTNAAVGAAYGCNAARMGN 60
Db 604 TCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGT 663
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Query Match	67.2%	Score 244	DB 4	Length 1472
Best Local Similarity	53.6%	Pred. No. 1.2e-65		
Matches 194	Conservative 97	Mismatches 71	Indels 0	Gaps 0

RESULT 14
US-09-438-046-1
; Sequence 1, Application US/09438046

1 COUNCIL OF THE UNIVERSITY OF TORONTO
2
3 / APPLICANT: ERIKSSON, Ulf
4 / APPLICANT: AASE, Karin
5 / APPLICANT: LEE, Xuri
6 / APPLICANT: PONTN, Annica
7 / APPLICANT: UTELA, Marko
8 / APPLICANT: ALITALO, Kari
9 / APPLICANT: OESTMAN, Arne

Oy AATGTGGGNTGYGNACNGTNAAYTTGGGNGMSNNTGYACNTGYAAYWSNCGNAAACNGTN 225
 |||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 1 AATTGTGGCTGTGAAGACTGTCAACTGGAGGTCCTGCACATGCATAATCAGGAAAACCCTG 60

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; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6

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? ORGANISM: Artificial Sequence
?
? FEATURE:
? OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
? OTHER INFORMATION: 2
?
? FEATURES:
? NAME/KEY: misc_feature
? LOCATION: (1... (1035)
?

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OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match	30.5%;	Score 110.8;	DB 4;	Length 1035;
Best Local Similarity	67.5%;	Pred. No. 2.9e-24;		
Matches 224;	Conservative 17;	Mismatches 82;	Indels 9;	Gaps 1;

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTMCACNARGARGRTMGNNTNTATYMSNTGYACCCCMGNAATTTT 765

QY 85 WNSGTNAAYATTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAATHTTGTGGCCGNGTGYTN 825

QY 145 YTGTCARCMTGYGANGGNAAYTGCGNTGYGNAACNGTNAAYTGCMGMSNTGYACN 204

Db 826 YTGNTAARMGNTGYGANGGNAAYTGCGNTGYTNTTCAYAAITGYAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARTTAYCAYARGTNTTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTGCCMSNAARTTNAACNAARAARTTAYCAYARGTNTTNCARTTNGMGC----- 938

QY 265 ATAAEMGNMGNGMNGCNAARAACNATGGCNTYNGTNGAYATCARTYNTNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEAGMTGYGATGYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

Query Match	30.5%;	Score 110.8;	DB 4;	Length 1035;
Best Local Similarity	67.5%;	Pred. No. 2.9e-24;		
Matches 224;	Conservative 17;	Mismatches 82;	Indels 9;	Gaps 1;

Query Match	30.5%;	Score 110.8;	DB 4;	Length 1035;
Best Local Similarity	67.5%;	Pred. No. 2.9e-24;		
Matches 224;	Conservative 17;	Mismatches 82;	Indels 9;	Gaps 1;

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTAYMSGTACACCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTAYMSNTGYACCMGNAATTTT 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAHTTTTGTGCGCGAGTGYTN 825

QY 145 YTGTCNARMGNTGYGANGANAAYTGCGNTGYGNAACNGTNAAYTGGMGMSNTGYACN 204

Db 826 YTGNTNAARMGNTGYGANGNAAYTGYGNTGYTYTNCAYAAITGYAAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARTAYCAYGARGTNTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCMWSNAARTTNAACNAARAARTAYCAYGARGTNTNCARTYMGNC----- 938

QY 265 ATAAEMGNMGNGMNGCNAARAACNATGGCNTYNGTNGAYATHCARTYNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEAGNTGYGATGYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTACACCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTATYMSNTGYACCMGNAATTTT 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAHTTTTGTGGCCGAGTGYTN 825

QY 145 YTGTCARCAGNTGYGANGANAAYTGCGANTGYGNAACNGTNAAYTGGMGMSNTGYACN 204

Db 826 YTGNTNAARMGNTGYGANGNAAYTGYGNTGYTGYTNCAYYATGYAAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARTTAYCAYGARGTNTYTCARTTYGARCCNGNCAY 264

Db 886 TGTGTGCCMSNAARGTNACNAARAARTTAYCAYGARGTNTYTCARLYTMGNC----- 938

QY 265 ATAAAEAGMGNGMGNGCNAARAACNATGGCAGTNGTNGAYATACARYTNGAYCAYCA 324

Db 939 --NAADACNGAGTMMNGAGTNTNCAAYAAASNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEMGTGTGATGTGYATHTGYSMNSNNGNC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTMCNARGARGRTMGNNTNTATWMSNTGYACCCCMGNAATTTT 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAATHTTGTGGCCGAGTGYTN 825

QY 145 YTGTCARCAGNTGYGANGANAAYTGCGANTGYGNAACNGTNAAYTGGMGMSWNTGYACN 204

Db 826 YTGNTAARMGNTGYGANGNAAYTGYGNTGYTGYTNCAVAAITGYAAVGAARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARATYACVARGTNTYTCARTTYGARCCNGNCAY 264

Db 886 TGTGTGCCWMSNAARTTNACNAARAATYACVARGTNTYTCARLYTMGNC----- 938

QY 265 ATAAATMGNGMGNGMNGCNAARACNAATGGCANTYNGTNGAYATHCARYTNGAYCAVCA 324

Db 939 --NAADACNGAGTMMNGAGTYTNCAYAAARSNTYTNACMGAYGTNGCNYTNGARCAVCA 996

QY 325 GAEMNTGYGATGYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTAYMSNTGYACCCCMGNAATTTT 765

QY 85 WNSGTNAAYATTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTNN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAATHTTGTGGCCGNGTGYTNN 825

QY 145 YTGTCNARMGNTGYGNGGNAAYTGYGNTTGGNACNGTNAAYTGGMGMSNTGYACN 204

Db 826 YTGNTNAARMGNTGYGNGGNAAYTGYGNTGYTNTTCAYAAITGYAAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARATTAAYCAYARGTNTTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCCMWSNAARGTNACNAARAARATTAAYCAYARGTNTTNCARYTMGNC----- 938

QY 265 ATAAAEAMGNMGNGMNGCNAARAACNATGGCNTYNGTNGAYATACARYTNGAYCAY 324

Db 939 --NAADACNGNGTMMNGNGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEMNTGTGATGTATATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNCANAGARGRTMGNTINTAYMSGTGACCCCMGNAATTTT 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAHTTTTGTGGCCMGNTGYTN 825

QY 145 YTGTCARCMTGYGANGGNAAYTGCGNTGYGNAACNGTNAAYTGCMGMSVSTGACN 204

Db 826 YTGNTNAARMGNTGYGANGGNAAYTGCGNTGYTNTNCAYAAITGYAAVAGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARTAYCAYGARGTNTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCMWSNAARTTNCNAARAARTAYCAYGARGTNTNCARTYMGNC----- 938

QY 265 ATAAATMGNGMGNGMNGCNAARAACMTAGCGTNTNGAYATACARYTNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNCACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAGMNTGTGATGTAYATHGTYSMSNSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTACACCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTATYMSNTGYACCMCGNAATTTY 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAHTTTYTGCCCGAGNTGYTN 825

QY 145 YTGTCARCAGNTGYGANGANAAYTGCGNTTGGNACNGTNAAYTGGMGMSWNTGYACN 204

Db 826 YTGNTNAARMGNTGYGANGNAAYTGYGNTGYTGYTNCAYYATGYAAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARATYACAYARGTNTYTCARTTYGARCCNGNCAY 264

Db 886 TGTGTGCCWMSNAARTTNAACNAARAATYACAYARGTNTYTCARLYTMGNC----- 938

QY 265 ATAAATMGNGMGNGMNGCNAARAACNATGGCNTYNGTNGAYATGARCAYTNGAYCAY 324

Db 939 --NAADACNGNGTMMNGNGNTTNCAYAARMSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEMNTGTGATGTGYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTAYMSNTGYACCCCMGNAATTTT 765

QY 85 WNSGTNAAYATTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAATHTTGTGGCCGNGTGYTN 825

QY 145 YTGTCNARMGNTGYGNGGNAAYTGYGNTTGGNACNGTNAAYTGGMGMSNTGYACN 204

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QY 205 TGTAAATWSNGNAARACNGTNAARAARATYACARGTNTTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCCMWSNAARGTNACNAARAARATYACARGTNTTNCARYTMGNC----- 938

QY 265 ATAAEMGNMGNGMNGCNAARAACNATGGCNTYNGTNGAYATCARYYTNGAYCAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEAGMTGTGATGTYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTATYMSNTGYACCCCMGNAATTTT 765

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Db 826 YTGNTNAARMGNTGYGNGGNAAYTGYGNTGYTNTTCAYAAITGYAAVGYARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARTTAYCAYARGTNTTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCCMWSNAARTTNAACNAARAARTTAYCAYARGTNTTNCARTTNGMGC----- 938

QY 265 ATAAATMGNGMGNGMNGCNAARAACNATGGCNTTNGATYATHCARTTNGAYCAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNTTNGARCAICAY 996

QY 325 GAGMNTGTGATGTATHTGTYSMSNSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTATYMSNTGYACCCCMGNAATTTT 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAATHTTGTGGCCGNGTGYTN 825

QY 145 YTGTCARCMTGYGANGGNAAYTGCGNTGYGNAACNGTNAAYTGCMGMSNTGYACN 204

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QY 205 TGTAAATWSNGNAARACNGTNAARAARTTAYCAYARGTNTTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTGCCMWSNAARTTNAACNAARAARTTAYCAYARGTNTTNCARTTNGMGC----- 938

QY 265 ATAAATMGNGMGNGMNGCNAARAACNATGGCNTYNGTNGAYATACARYTNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEMNTGTGATGTATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTACACCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTATYMSNTGYACCMCGNAATTTY 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

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QY 205 TGTAAATWSNGNAARACNGTNAARAARTTAYCAYGARGTNTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCMWSNAARTTNAACNAARAARTTAYCAYGARGTNTNCARTYMGNC----- 938

QY 265 ATAAEMGNMGNGMNGCNAARAACNATGGCNTYNGTNGAYATHCARTYNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEMNTGYGATGYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTTAYMSGTGACCCCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTMCACNARGARGRTMGNNTNTATYMSNTGYACCCCMGNAATTTT 765

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QY 145 YTGTCARCMTGTYGANGGNAAYTGCGNTTGGNACNGTNAAYTGCMGMSNTGYACN 204

Db 826 YTGNTNAARMGNTGYGNGGNAAYTGYGNTGYTNTTCAYAAITGYAAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARATYACARGTNTTNCARTTYGARCCNGNCAY 264

Db 886 TGTGTGCCMWSNAARGTNACNAARAARATYACARGTNTTNCARYTMGNC----- 938

QY 265 ATAAATMGNGMGNGMNGCNAARAACNATGGCNTYNGTNGAYATGARCNTYNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAICAY 996

QY 325 GAEMNTGTGATGTGATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

QY 25 GTGCAATTNCAATYAGNTTNAAYGAYGAYGCNAARMGNTAYMSGTACACCMGNAATAY 84

Db 706 GTMGCAATTNAAYTTNTTNAACNARGARGRTMGNNTNTAYMSNTGYACCMGNAATTTT 765

QY 85 WNSGTNAAYTTHGNGARGARTTNAARYTNGCNAAYGTNGTNTTYYYCCMGNTGYTN 144

Db 766 WNSGTWMSNATTHGNGARGARTTNAARMGNAACNGAYACNAHTTTTGTGGCCMGNTGYTN 825

QY 145 YTGTCNARMGNTGYGANGNAAYTGYGANTGYGNAACNGTNAAYTGGMGMSNTGYACN 204

Db 826 YTGNTNAARMGNTGYGANGNAAYTGYGNTGYTNTTCAYAAITGYAAAYGARTGYCAR 885

QY 205 TGTAAATWSNGNAARACNGTNAARAARTAYCAYGARGTNTTCARTTYGARCCNGNCAY 264

Db 886 TGTGTNCMWSNAARTTNAACNAARAARTAYCAYGARGTNTTCARLYTMGNC----- 938

QY 265 ATAAEMGNMGNGMNGCNAARAACNATGGCNTYNGTNGAYATGARCAYTNGAYCAY 324

Db 939 --NAADACNGNGTMMNGGNTTNCAYAAARSNTTNAACNGAYGTNGCNYTNGARCAYCAI 996

QY 325 GAEAGMTGYGATGYATHTGYMSNMSNNGCC 356

Db 997 GARGARTGYGATGYGTNTGYMGNGMNSNAC 1028

Search completed: November 15, 2004, 20:18:44
Job time : 47.8228 secs

Job time : 47.8228 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:58:20 ; Search time -611.407 Seconds
(without alignments)
-3116.645 Million cell updates/sec

Title: US-09-876-813-6_COPY_748_1110
Perfect score: 363
Sequence: 1 wantcaycagaymnaarws.....gywanwamngncncmgn 363

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261.6	72.1	369	10	ADK68115
2	261.6	72.1	620	4	ABA08941
3	261.6	72.1	881	9	AAD58401
4	261.6	72.1	1041	10	ADK68119
5	261.6	72.1	1110	3	AAFC8156
6	261.6	72.1	1110	4	AAFC24197
7	261.6	72.1	1110	10	ACA64110
8	261.6	72.1	1110	12	ADJ33759
9	261.6	72.1	1162	4	AAS82136
10	261.6	72.1	1162	6	AB188828
11	261.6	72.1	1162	6	AB195717
12	261.6	72.1	1162	8	ACA03695
13	261.6	72.1	1162	8	ABX89233
14	261.6	72.1	1162	8	ACD41887
15	261.6	72.1	1162	8	ACA04116
16	261.6	72.1	1162	9	ADA45704
17	261.6	72.1	1162	9	ADA76135
18	261.6	72.1	1162	9	ADA18785
19	261.6	72.1	1162	9	ADA61408
20	261.6	72.1	1162	9	ADB19193
21	261.6	72.1	1162	9	ADB27734

22	261.6	72.1	1162	9	ADA86213	Ada86213	Novel	hum
23	261.6	72.1	1162	9	ADB15777	ADB15777	Human	PRO
24	261.6	72.1	1162	9	ADA47563	ADA47563	Human	PRO
25	261.6	72.1	1162	9	ADA67358	ADA67358	Human	PRO
26	261.6	72.1	1162	9	ADB30365	ADB30365	CDNA	enco
27	261.6	72.1	1162	9	ADA85661	ADA85661	Novel	hum
28	261.6	72.1	1162	9	ADA96873	ADA96873	Human	PRO
29	261.6	72.1	1162	9	ADA79177	ADA79177	Human	PRO
30	261.6	72.1	1162	9	ADA87316	ADA87316	Novel	hum
31	261.6	72.1	1162	9	ADB16518	ADB16518	Human	PRO
32	261.6	72.1	1162	9	ADA91610	ADA91610	Novel	hum
33	261.6	72.1	1162	9	ADB14673	ADB14673	Human	PRO
34	261.6	72.1	1162	9	ADB18634	ADB18634	Novel	hum
35	261.6	72.1	1162	9	ADA93849	ADA93849	Human	PRO
36	261.6	72.1	1162	9	ADB19745	ADB19745	Novel	hum
37	261.6	72.1	1162	9	ADB13057	ADB13057	Human	PRO
38	261.6	72.1	1162	9	ACD98516	ACD98516	Novel	hum
39	261.6	72.1	1162	9	ADA74311	ADA74311	Human	PRO
40	261.6	72.1	1162	9	ADB24544	ADB24544	Human	PRO
41	261.6	72.1	1162	9	ADA82068	ADA82068	Human	PRO
42	261.6	72.1	1162	9	ADA75031	ADA75031	Human	PRO
43	261.6	72.1	1162	9	ADA85109	ADA85109	Novel	hum
44	261.6	72.1	1162	9	ADA84557	ADA84557	Novel	hum
45	261.6	72.1	1162	9	ADB29813	ADB29813	CDNA	enco

ALIGNMENTS

RESULT 1	ADK68115	ADK68115 standard; DNA; 369 BP.
ID	ADK68115	
AC	ADK68115;	
DT	06-MAY-2004 (first entry)	
XX		
DE	Novel NOVX gene #21.	
XX		
KW	ds; gene; antidiabetic; anorectic; cardiant; hypotensive;	
KW	antiarteriosclerotic; anorectic; vitruide; antibacterial; fungicide;	
KW	protozoacidal; neurotropic; neuroprotective; antiparkinsonian;	
KW	anticonvulsant; osteopathic; antiairchitic; antiinflammatory;	
KW	dermatological; antiastrumatic; antilipemic; gene therapy;	
KW	metabolic disorder; diabetes; obesity; infectious disease; anorexia;	
KW	cancer; cardiovascular disease; hypertension; atherosclerosis;	
KW	neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;	
KW	epilepsy; immune disorder; osteoarthritis; hematopoietic disorders;	
KW	inflammatory skin disorder; asthma; dyslipidemia; neurogenesis;	
KW	cell differentiation; cell proliferation; hematopoiesis; wound healing;	
KW	angiogenesis; chromosome mapping; pharmacogenomic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003085124-A2.	
XX		
PD	16-OCT-2003.	
XX		
PF	01-APR-2003; 2003WO-US009775.	
XX		
PR	01-APR-2002; 2002US-0369065P.	
PR	05-APR-2002; 2002US-0370279P.	
PR	05-APR-2002; 2002US-0370359P.	
PR	08-APR-2002; 2002US-0370969P.	
PR	12-APR-2002; 2002US-0372019P.	
PR	22-APR-2002; 2002US-0374379P.	
PR	15-MAY-2002; 2002US-0380973P.	
PR	30-MAY-2002; 2002US-0384297P.	
PR	30-MAY-2002; 2002US-0384329P.	
PR	17-JUN-2002; 2002US-0389729P.	
PR	13-AUG-2002; 2002US-0403491P.	
PR	15-AUG-2002; 2002US-0403748P.	
PR	31-MAR-2003; 2003US-00403142.	

XX (CURA-) CURAGEN CORP.
 PA
 XX

PI Alschbrook JP, Bento P, Boldog FL, Burgess CE, Casman SJ,
 PI Crabtree-Bokor JR, Edinger SR, Elletman K, Fernandes ER, Gerlach VL,
 PI Grosse WM, Gunther E, Gunse VY, Heyes MP, Lepley DW, Li L,
 PI Macdougall JR, Malyankar UM, Millet I, Paturajan M, Peyman JA,
 PI Rastelli L, Rieger DK, Shenoy SG, Shinkets RD, Smithson G, Stone DJ,
 PI Vernet CAM, Voss EZ;

DR MPI; 2003-812730/76.
 DR P-PSDB; ADK68116.

PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.

PS Claim 20; SEQ ID NO 41; 323bp; English.

XX The invention relates to novel NOVX protein and their encoding DNA's,
 CC mature forms of the proteins or sequences that are at least 95% identical
 CC to, or having one or more conservative amino acid substitutions in, the
 CC proteins. The polypeptides, nucleic acid molecules and antibodies are
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOVX-associated disorder.
 CC The nucleic acid molecules, polypeptides and antibodies are useful for
 CC treating, preventing or diagnosing diseases such as metabolic disorders,
 CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
 CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
 CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
 CC disease, Parkinson's disease, epilepsy, immune disorders
 CC (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
 CC asthma, and various dyslipidemias. The nucleic acids and polypeptides may
 CC also be used as targets for the identification of small molecules that
 CC modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC corresponds to one of the NOVX genes of the invention.

XX Sequence 369 BP; 102 A; 80 C; 100 G; 87 T; 0 U; 0 Other;

Query Match 72.1%; Score 261.6; DB 10; Length 369;
 Best Local Similarity 56.6%; Pred. No. 3.9e-62;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 MSNTRAYCAYGVMGNMNAARWMSNAARGTNGAYTTNGAYGNTNAAAYGAYGCAAPMGN 60
 Db 7 TCATTCACATGACCGGAGTCAAAAGTTGACCTGATGAGGCTCATGTATGCAAGCGT 66

QY 61 TAYVSNTRYACNCCNMGNAATYATYVTHNGNGBRGARVYNARVYNGNAAAY 120
 Db 67 TAGAGTTGCACTCCAGAGAAATTAATCGCTCAATTAAGAAAGAGCTGAAGTTGGCCAAT 126

QY 121 GTNCTNTTYYCCNMGNTGYTYTYNTNGTNCARMNGTYGNGGNAAYTYGNTGYG 180
 Db 127 GTGTCTCTCTTCCACCTTGCTCTCTGTCAGCGCTGTGAGGAAATTTGTGCTGTGGA 186

QY 181 ACNGTNAAYGAGMGNMNTGYACNTGYAAYVMSNGNAAACNGTNAARARATYCAVGAR 240
 Db 187 ACTGTCACTGAGAGTCTCTGCACTGCAATTCAGGAAAAACCGTGAAGAAAGTTCATGAG 246

QY 241 GTNNTTCARTTYGARCCNNGNCAYATTAAMGNMNGNMGNCNAAACATGATGCTG 300
 Db 247 GTATTACAGTTTGAAGCTGCGCACATCAAGAGAGGGGTGAGACTTAAGACCAATGGCTCTA 306

QY 301 GTTGAAVTHGARTNGAYTCAVYAGVAMGNTGYGATGTATTTGYVSNMNGNCCN 360
 Db 307 GTTGACATCCAGTTGATYACCATGAACGATGTGATGTATCTGACAGTCAAGACCACT 366

QY 361 MG 362
 Db 367 CG 368

RESULT 2
 ID ABA08941 standard; cDNA; 620 BP.

ABA08941;

11-JAN-2002 (first entry)

Human novel protein-encoding cDNA, SEQ ID NO.717.

Human; cytokine; cell proliferation; cell differentiation; growth factor;
 haematopoiesis regulation; tissue growth; immunomodulator; activin;
 inhibin; chemotaxis; chemokinesis; cancer; tumour; haematopoietic disorder;
 myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 chronic inflammatory condition; proliferative retinopathy;
 atherosclerosis; coronary heart disease; arterial ischaemia;
 bone disorder; osteoporosis; vascular growth disorder;
 tissue regeneration; wound healing; infection; immune disorder;
 cell culture; drug screening; gene therapy; antiinflammatory;
 antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 cyostatic; osteopathic; vasotropic; cardiant; virocidic; antibacterial;
 antifungal; vulnery; antitumor; ss.

XX Homo sapiens.

XX W0200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX MPI; 2001-457740/49.

XX P-PSDB; ABB1697.

XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.

PS Claim 1; Page 656; 1963bp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities, stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness.
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX

SQ Sequence 620 BP; 179 A; 135 C; 153 G; 153 T; 0 U; 0 Other;

Query Match 72.1%; Score 261.6; DB 4; Length 620;

Best Local Similarity 56.6%; Pred. No. 5.3e-62;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGYMGNAAARWSNARGTNGAYYTNAGYMGNTNAAVGAAYGACNAARMGN 60
DB TCATACCATGACCGGAAGTCAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGGT 155
QY 61 TAYVNSTGYACNCCMGNAAVTAWSNGTNAAYATHMNGARGARYTNAARYTNGCNAAY 120
DB 156 TACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAT 215

QY 121 GTNGTNTTYYTCCMGNTGYTYNTNGTNCARMGNTGYGNGNAAVTGNGTYGNGN 180
DB 216 GTGTCCTCTTCCACGTTGCTCCTCGTGACGGCTGTGAGGAAATTTGGCTGTGA 275

QY 181 ACNGTNAAYTSGMGMSNTGYACNTGYAAYVNSNGNABARACNGTNAARATATAYCAYGAR 240
DB 276 ACTGTCAACTGGAAGTCTCTGCACATGCAATTCAGGGAAAACCGTGAATAATCATAG 335

QY 241 GTNYTNCARTTYGARCCNGNCAYATHAARMNGNMGNGCNAARACNATGCGNYTN 300
DB 336 GTATTACAGTTTGAGCCTGGCCATCAAGAGAGGGGTAGAGCTAAGACCATGGCTCTA 395

QY 301 GTNGAYATHCARRYTNGAYCAYCAGARMGNTGYATYATHTGYMSWMSMGNCNCN 360
DB 396 GTTGACATCCAGTTGATGATCACCATGAACGATGTGATCTGCAAGCTCAAGACCACT 455

QY 361 MG 362
DB 456 CG 457

RESULT 3
AADS8401
ID AADS8401 standard; DNA; 881 BP.

AC AADS8401;
XX 20-NOV-2003 (first entry)

XX pTPP339 insert DNA used in the exemplification of the invention.
XX Platelet-derived growth factor-D; PDGF-D; bone graft; osteopathic;
XX radiation-induced osteonecrosis; periodontal disease; protein therapy;
XX joint injury; osteoporosis; bone loss; fracture; bone healing; ds..
XX Unidentified.

XX OS
XX PN WO2003068802-A2.
XX PD 21-AUG-2003.

PF 11-FEB-2003; 2003WO-US004213.

XX 11-FEB-2002; 2002US-0355882P.

XX (ZYMO) ZYMOGENETICS INC.

XX Fox BA, Moore MD, Swiderk KM, Birks CW;

XX WPI; 2003-646473/61.

XX New fusion protein comprising a first platelet-derived growth factor-D
XX (PDGF-D) domain, a linker, and a second PDGF-D domain polypeptides,
XX useful for stimulating the production of bone and/or connective tissue.

XX Example 5; Page 48; 50pp; English.

XX The invention relates to a fusion protein comprising, from amino to
XX carboxyl terminus, a first platelet-derived growth factor-D (PDGF-D)
XX domain polypeptide, a linker polypeptide, and a second PDGF-D domain
XX polypeptide. The fusion proteins are useful for stimulating the
XX production of bone and/or connective tissue in both human and non-human
XX animals. The fusion proteins are specifically useful in non-union
XX fractures and fractures in patients with compromised healing, bone
XX grafts, bone healing following radiation-induced osteonecrosis, implants,
XX or treatment of periodontal disease, joint injuries, osteoporosis or
XX other conditions characterised by increased bone loss or decreased bone
XX formation. The invention is useful in protein therapy. The present
XX sequence is pTPP339 insert DNA used in the exemplification of the
XX invention. PDGF-D is known as zveg14

SQ Sequence 881 BP; 246 A; 185 C; 228 G; 222 T; 0 U; 0 Other;

Query Match 72.1%; Score 261.6; DB 9; Length 881;

Best Local Similarity 56.6%; Pred. No. 6.6e-62;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGYMGNAAARWSNARGTNGAYYTNAGYMGNTNAAVGAAYGACNAARMGN 60
DB 105 TCATACCATGACCGGAAGTCAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGGT 164

QY 61 TAYVNSTGYACNCCMGNAAVTAWSNGTNAAYATHMNGARGARYTNAARYTNGCNAAY 120
DB 165 TACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAT 224

QY 121 GTNGTNTTYYTCCMGNTGYTYNTNGTNCARMGNTGYGNGNAAVTGNGTYGNGN 180
DB 225 GTGTCCTCTTCCACGTTGCTCCTCGTGACGGCTGTGAGGAAATTTGGCTGTGA 284

QY 181 ACNGTNAAYTSGMGMSNTGYACNTGYAAYVNSNGNABARACNGTNAARATATAYCAYGAR 240
DB 285 ACTGTCAACTGGAAGTCTCTGCACATGCAATTCAGGGAAAACCGTGAATAATCATAG 344

QY 241 GTNYTNCARTTYGARCCNGNCAYATHAARMNGNMGNGCNAARACNATGCGNYTN 300
DB 345 GTATTACAGTTTGAGCCTGGCCATCAAGAGAGGGGTAGAGCTAAGACCATGGCTCTA 404

QY 301 GTNGAYATHCARRYTNGAYCAYCAGARMGNTGYATYATHTGYMSWMSMGNCNCN 360
DB 405 GTTGACATCCAGTTGATGATCACCATGAACGATGTGATCTGCAAGCTCAAGACCACT 464

QY 361 MG 362
DB 465 CG 466

RESULT 4
ADK68119
ID ADK68119 standard; DNA; 1041 BP.

XX ADK68119;
XX 06-MAY-2004 (first entry)

DE Novel NOVX gene #23.
XX
XX de; gene: antidiabetic; anorectic; cardiant; hypotensive;
KM arteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KM protocoal; neurotrophic; neuroprotective; antiparkinsonian;
KM anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KM dermatological; antiaesthetic; antileptic; gene therapy;
KM metabolic disorder; diabetes; obesity; infectious disease; anorexia;
KM cancer; cardiovascular disease; hypertension; atherosclerosis;
KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KM epilepsy; immune disorder; osteoarthritis; hematopoietic disorders;
KM inflammatory skin disorder; asthma; dyslipidemia; neurogenesis;
KM cell differentiation; cell proliferation; hematopoiesis; wound healing;
KM angiogenesis; chromosome mapping; pharmacogenomic.
XX
XX Homo sapiens.
XX
XX MO2003085124-A2.
XX
XX 16-OCT-2003.
XX
XX 01-APR-2003; 2003WO-US009775.
XX
XX 01-APR-2002; 2002US-0369065P.
XX
XX 05-APR-2002; 2002US-0370279P.
XX
XX 05-APR-2002; 2002US-0370359P.
XX
XX 08-APR-2002; 2002US-0370969P.
XX
XX 12-APR-2002; 2002US-0372019P.
XX
XX 22-APR-2002; 2002US-0374379P.
XX
XX 15-MAY-2002; 2002US-0380973P.
XX
XX 30-MAY-2002; 2002US-0384297P.
XX
XX 30-MAY-2002; 2002US-0384329P.
XX
XX 17-JUN-2002; 2002US-0389729P.
XX
XX 13-AUG-2002; 2002US-0403491P.
XX
XX 15-AUG-2002; 2002US-0403748P.
XX
XX 31-MAR-2003; 2003US-00403142.
XX
XX (CURA) CURAGEN CORP.
XX
XX Alabreck JP, Bento P, Boldog FU, Burgess CE, Casman SJ;
PI Crabtree-Bokor JR, Edinger SR, Ellerman K, Fernandes ER, Gerlach VL;
PI Grosse WM, Gunther B, Gusev VY, Hayes MP, Lesley DM, Li L;
PI Macdougall JR, Malysankar UM, Miller I, Paturajan M, Peyman JA;
PI Rastelli L, Rieger DK, Shenoy SG, Shimkels RD, Smltson G, Stone DJ;
PI Vernet CM, Voss Ez;
XX
XX WPI; 2003-812730/76.
XX
XX P-PSDB; ADK68120.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 20; SEQ ID NO 45; 323pp; English.
XX
XX The invention relates to novel NOVX protein and their encoding DNA's,
XX mature forms of the proteins or sequences that are at least 95% identical
XX to, or having one or more conservative amino acid substitutions in, the
XX proteins. The polypeptides, nucleic acid molecules and antibodies are
XX useful in the manufacture of a medicament for treating a syndrome
XX associated with a human disease, preferably a NOVX-associated disorder.
XX The nucleic acid molecules, polypeptides and antibodies are useful for
XX treating, preventing or diagnosing diseases such as metabolic disorders,
XX diabetes, obesity, infectious diseases (viral, bacterial, fungal,
XX helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
XX (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
XX disease, Parkinson's disease, epilepsy, immune disorders
XX (osteoarthritis), hematopoietic disorders, inflammatory skin disorders,
XX asthma, and various dyslipidemias. The nucleic acids and polypeptides may
XX also be used as targets for the identification of small molecules that
XX modulate or inhibit e.g. neurogenesis, cell differentiation, cell
XX proliferation, hematopoiesis, wound healing and angiogenesis, in gene

CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX genes of the invention.
XX
SQ Sequence 1041 BP; 314 A; 233 C; 250 G; 244 T; 0 U; 0 Other;
Query Match 72.1%; Score 261.6; DB 10; Length 1041;
Best Local Similarity 56.6%; Pred. No. 7,4e-62;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;
QY 1 MSNTAYCAAGYMGNAARWNAARCTNGAYTNGAYGNTNAAAYGAYGCAARWGN 60
DB 679 TCATACCATGACCGGAAGTCAAAAGTACCTGATGCTCAATGATGACCAAGCT 738
QY 61 TAYWNTGYACNCCNMGNAAYTAYWNTGNAAYATHTNGARGARYNARNTNGNAAY 120
DB 739 TACAGTTCACCTCCAGAAATTAAGTCTCAATATTAAGAGAGAGCTGAAGTGGCCAT 798
QY 121 GTNGTNTTYYTCCNMGNTGYTNTGNTNCAWNTGYGNGNAAAYTGYGNTGYGN 180
DB 799 GTGCTCTTCTTCCAGCTGCTCCTGCTGACGCGTGTGAGGAATTTGTGCTGTGGA 858
QY 181 ACGTNAAYTGGGNNSTNGAYACNTGYAAYWNGNAAACNGTNAARATYCAAGAR 240
DB 859 ACTGTCACTGAGAGTCTGACATCAATTCAGGAAAAACCTGAAAAAGTATCATGAG 918
QY 241 GTWYTCARTTYGACCGNGNCAYATTAARMGNGMNGMNGNCNARACNATGGGNYN 300
DB 919 GTATTACAGTTTGAAGCTGCGCACATCAAGAGAGGGGTAGAGCTAAGACATGCTCTA 978
QY 301 GTNGAATATGARTNGAYCAAYCAAGRMGNTGYGAYTATHTGWSNNMNGNCCN 360
DB 979 GTTGACATCCAGTTGATCAATGAAGATGATGATGTGACGTCAAGACCACT 1038
QY 361 MG 362
DB 1039 CG 1040
RESULT 5
AAC81556
ID AAC81556 standard; DNA; 1110 BP.
XX
XX AAC81556;
XX
XX 09-MAR-2001 (first entry)
XX
XX Human growth factor homologue zvegf4 degenerate DNA, SEQ ID NO:6.
XX
XX Human; zvegf4; growth factor homologue; VEGF/PDGF family; CUB domain;
XX PDGF-like activity; mitogenic; osteogenic; neovascularisation;
XX tissue repair; proliferation; differentiation; liver damage;
XX neurodegenerative; Alzheimer's disease; multiple sclerosis;
XX periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
XX immunomodulation; hepatic; ds.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200066736-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US040047.
XX
XX 03-MAY-1999; 99US-00304216.
XX
XX 10-NOV-1999; 99US-0164463P.
XX
XX 04-FEB-2000; 2000US-0180169P.
XX
XX (ZYMO) ZYMOGENETICS INC.

PA (GILB/) GILBERTSON D G.
XX
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
DR WPI; 2004-070738/07.
XX
PT New zvegff4 polypeptides and nucleic acids, useful for diagnosing or
PT treating cell loss or abnormal cell proliferation, e.g. cancer, treating
PT full-thickness skin wounds or treating female reproductive tract
PT disorders.

Claim 34; SEQ ID NO 6; 73bp; English.

CC The invention relates to growth factor homologue zvegff4, its
CC corresponding nucleic acid and methods of using them. The sequences of
CC the invention are used in the study and regulation of cell and tissue
CC development, as components of cell culture media and as diagnostic
CC agents. The zvegff4 polypeptide can be used in treating full-thickness
CC skin wounds, including venous stasis, ulcers and other chronic, non-
CC healing wounds, in fracture repair, skin grafting, in constructive
CC surgery to promote neovascularisation and increase skin flap survival, to
CC establish vascular networks in transplanted cells and tissues, or in
CC treating female reproductive tract disorders, including acute or chronic
CC placental insufficiency and prolonged bleeding. It can also be used to
CC promote endothelialisation of vascular grafts and stents, in treating
CC acute or chronic lesions of the gastrointestinal tract or treating or
CC repairing liver damage. Zvegff4 can also be used for treating hepatic
CC chronic passive congestion (CPC) and central haemorrhagic necrosis (CHN).
CC Zvegff4 proteins, agonists and antagonists can also be used to modulate
CC neurite growth and development and demarcate nervous system structures.
CC It can also be used for treating peripheral neuropathies or
CC neurodegenerative diseases including multiple sclerosis, Alzheimer's
CC disease or Parkinson's disease. The polypeptides, nucleic acids and
CC antibodies can also be used to diagnose or treat disorders associated
CC with cell loss or abnormal cell proliferation (including cancer). The
CC invention is useful in gene therapy. The present sequence is human zvegff4
CC degenerate DNA.

XX Sequence 1110 BP; 215 A; 94 C; 178 G; 139 T; 0 U; 484 Other;

Query Match 72.1%; Score 261.6; DB 12; Length 1110;

Best Local Similarity 100.0%; Pred. No. 7,7e-62;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WSNATYCAYGAYMGAAWMSNARGTNGAYTNGAYMGNTYMAAGAYGCNAARNGN 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 748 WSNATYCAYGAYMGAAWMSNARGTNGAYTNGAYMGNTYMAAGAYGCNAARNGN 807
QY 61 TAYMSNTGYACNCGMGNAAATAYMSNGTNAAYATHMNGARGARYTAAAYTNGCNAY 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 808 TAYMSNTGYACNCGMGNAAATAYMSNGTNAAYATHMNGARGARYTAAAYTNGCNAY 867
QY 121 GTNGNTTYYTCCMNGTGYTNTYNTGNCARMGNTGYGNGNAAAYTGCGNTGYGN 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 868 GTNGNTTYYTCCMNGTGYTNTYNTGNCARMGNTGYGNGNAAAYTGCGNTGYGN 927
QY 181 ACNGTNAAYTSGMGWSTGYACTGYAAYMSNGNAAARACNGTAAABAARTAYAYGAR 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 928 ACNGTNAAYTSGMGWSTGYACTGYAAYMSNGNAAARACNGTAAABAARTAYAYGAR 987
QY 241 GTNTYNTGARTTYGARGCNGNCAVATTHAARMGNGMNGNCAARACNATGCGCNTN 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 988 GTNTYNTGARTTYGARGCNGNCAVATTHAARMGNGMNGNCAARACNATGCGCNTN 1047
QY 301 GTNGAYATHCARNTYNGAYCAYCAYGARMGNTGYATGYATHGYTWSMNGNCGNCCN 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1048 GTNGAYATHCARNTYNGAYCAYCAYGARMGNTGYATGYATHGYTWSMNGNCGNCCN 1107
QY 361 MG 362
DB ||||
DB 1108 MG 1109

RESULT 9
AAS21336
ID AAS21336 standard; cDNA; 1162 BP.
XX
AC AAS21336;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO4345 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy; ss.
XX
OS Homo sapiens.
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PR 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99WO-US0170262P.
PR 16-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000276.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GENTH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerlicien ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12264.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect

PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Garlitsen WE, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-332040/31.
XX P-PSDB; ABU66662.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
XX therapy, in chromosome and gene mapping, as chromosome markers, in tissue
XX typing, and in chromosome identification.
XX
XX Claim 2; Fig 185; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for
XX identifying agonists or antagonists. The PRO polypeptides are useful for
XX for stimulating the release of tumour necrosis factor (TNF)-alpha from
XX human blood, for stimulating the proliferation or differentiation of
XX chondrocytes, and detecting the presence of tumours. The polynucleotide
XX sequences encoding PRO polypeptides are useful as hybridisation probes,
XX in chromosome and gene mapping, in the generation of antisense RNA and
XX DNA, in the preparation of PRO polypeptides, for generating transgenic
XX animals or knockout animals, for the genetic analysis of individuals with
XX genetic disorders, and in gene therapy. ACAA03603-ACAA03877 represent cDNAs
XX encoding the human PRO polypeptides of the invention. Note: The sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/patident.html
SQ Sequence 1162 BP; 342 A; 266 C; 276 G; 278 T; 0 U; 0 Other;
Query Match 72.1%; Score 261.6; DB 8; Length 1162;
Best Local Similarity 56.6%; Pred. No. 7,9e-62;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;
QY 1 MSNTAYCAYGAYMGNAARMSNAARGTNGAYVYTGAYMGNYTNAAYGAYGAYGNAARMGN 60
DB 761 TCATRCATGACGGAAGTCAAAAGTTGACCTGATAGGCTCATGATGATGCCAGGCT 820
QY 61 TAYWSNTGYACNCCNMGNAAATYAVWSNGTNAAYATHTMNGARGARYTNARATYNGCNAY 120
DB 821 TACAGTTGACATCCCAAGGAAATTAATCGGTCAATATTAAGAAAGAGCTGAGTGGCCAT 880
QY 121 GTNGNTTYTTCGCMGNTGYTNTNGTCARMENTGVGNGNAAATYTGANTGYGNN 180
DB 881 GTGGCTCTTCTTCCACGCTTGCTCTCTGTCGACGCTGTGAGGAAATTTGGCTGTGA 940
QY 181 ACNGTNAAYTGGMGWSNTGYACNTGYAAYWSNGNNAARACNGTNAARAAATYACAYGAR 240
DB 941 ACTGTCAACTGAGAGTCTGTGACATGCAATTCAGGAAACCGTCAAAAAGTATATATAG 1000
QY 241 GTNTYTCARTTYGARCCNGNCAYATHAARMGNMNGNMGNCNAPARACNATGGCNVYN 300
DB 1001 GTATTACAGTTGAGCCTGGCCACATCAAGAGAGGGGTAGAGCTAAGACATGCTCTA 1060
QY 301 GTNGAYTAHCHARYTNGACAYCAYGARMGNTGYATYTAHTTGYWSMWSMNGNCNCCN 360
DB 1061 GTTGACATTCAGTTGATCAACATGAGATGCGATTTGTATCTGCACTCAAGACCACT 1120
QY 361 MG 362

DB 1121 CG 1122
RESULT 13
ABX89233
ID ABX89233 standard; cDNA; 1162 BP.
XX
XX AC ABX89233;
XX
XX DT 13-MAY-2003 (first entry)
XX
XX DE DNA encoding novel secreted and transmembrane protein PRO4345.
XX
XX Human: PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
XX cardiac insufficiency disorder; cancer; tumour; immune response;
XX adrenal cortical capillary endothelial growth; c-fos induction;
XX vascular endothelial growth factor inhibition; VEGF inhibition;
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;
XX retinal neurons cell survival; rod photoreceptor cell survival;
XX retinal disorder; retinitis pigmentosa; kidney disorder;
XX mammalian kidney mesangial cell proliferation; Berger disease;
XX dematiitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2003017563-A1.
XX
XX PD 23-JAN-2003.
XX
XX PF 07-MAY-2002; 2002US-00140808.
XX
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022391.
XX 29-OCT-1998; 98WO-US022392.
XX 20-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028651.
XX 02-DEC-1999; 99WO-US028654.
XX 02-DEC-1999; 99WO-US028655.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 22-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US0000219.
PR 06-JAN-2000; 2000MO-US0000277.
PR 06-JAN-2000; 2000MO-US000376.
PR 11-FEB-2000; 2000MO-US0003565.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US004914.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005746.
PR 10-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006319.
PR 20-MAR-2000; 2000MO-US006884.
PR 21-MAR-2000; 2000MO-US007377.
PR 30-MAR-2000; 2000MO-US007532.
PR 17-MAY-2000; 2000MO-US008439.
PR 22-MAY-2000; 2000MO-US013705.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023528.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US034725.
PR 20-DEC-2000; 2000MO-US034958.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001MO-US006520.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001MO-US017032.
PR 01-JUN-2001; 2001US-00817803.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001MO-US019682.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001MO-US020116.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

XX (GETH) GENENTECH INC.

XX Baker KP, Baresini M, DeForge L, DeMayers L, Filvaroff E, Gao W,
PI Gerlesen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-148238/14.
XX P-PSDB; ABUS9743.

XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
XX and/or cartilage disorders, e.g. arthritis.

PS Claim 2; Fig 185; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO134 and PRO186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068, PRO137 and PRO1387 induce c-fos in
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and angiogenesis of this polypeptide are
CC useful for treating cancerous tumors. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumor growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein

XX Sequence 1162 BP; 342 A; 266 C; 276 G; 278 T; 0 U; 0 Other;

Query Match 72.1%; Score 261.6; DB 8; Length 1162;

Best Local Similarity 56.6%; Pred. No. 7,9e-62; Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WNSTAYCAGATMGNAARMSNARGTNGAYTNGAYMGNTYNAAYGAYGCNAAARMGN 60
DB 761 TCAATACCATGACCGGAAGCAAAAGTTGACCTGATGCTCAATGATGATGCCAAGCT 820
QY 61 TAYMSITGYACNCCNMGNNAATYAYMSNGTNAAYTHMGNGARGAYTAARTCNAY 120
DB 821 TACAGTTGACATCCAGAAATTAATCTCGCTCAATTAAGAAAGAGCTGAAGTGGCCAAAT 880
QY 121 GTNGNTTATTTTCNMGNTGYTNTNGTNCARMGNTGYGNGNAAYTGYGNTGYGN 180
DB 881 GTGGCTCTCTTCCACGTTGCTCTCGTGCAGCGCTGTGAGGAATTTGGCTGTGGA 940
QY 181 ACNGTNAAYTGMGMSNTGYACNTGYAAYMSNGNARACNGTNAAPAAATAYCARGAR 240
DB 941 ACTGTCAACTGAGAGGTCTCTGACATGACATTAAGGAAACCGTGAATAATATCTATAG 1000
QY 241 GTNTYTCARTTGYARCCNGNCAVATHAARMGNGMNGMNGCNAAACATGGCANTYN 300
DB 1001 GTATTACAGTTTGAACCTGGCCATCAATCAAGAGGGGTATAGCTAAGACCATGGCTTA 1060
QY 301 GTNGAYATHCARNTNGAYCAYCAYGARMGNTGYAYTGYATHTGYSWMSNMGCCNCCN 360
DB 1061 GTTGACATTCAGTTGATGATCACCATGAACGATGCATGTATCTCAGCTCAAGACCACT 1120
QY 361 MG 362
DB 1121 CG 1122

RESULT 14

ACD41887

ID ACD41887 standard; cDNA; 1162 BP.

XX AC ACD41887;

DT 05-SEP-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) cDNA #93.
XX
XX Human, *8q*; gene; PRO; secreted protein; transmembrane protein; tumour;
XX cytosolic; gene therapy; tumour necrosis factor- α ; TNF- α ; blood;
XX proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
XX BMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
XX chondrocyte cell proliferation; chondrocyte cell differentiation;
XX pericyte cell; inner ear utricle supporting cell; T-lymphocyte cell;
XX endothelial cell; A-peptide; factor VIIA.
XX
XX Homo sapiens.
XX
XX US2003036179-A1.
XX
XX 20-FEB-2003.
XX
XX 10-MAY-2002; 2002US-00142431.
XX
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 29-OCT-1998; 98WO-US022992.
XX 20-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005130.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 22-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005746.
XX 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032578.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00928072.
XX
XX (GERTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-466355/44.
XX P-PSDB; ABO24933.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
XX PRO4978, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 2; Fig 185; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 80%
XX sequence identity to a PRO (secreted and transmembrane protein) cDNA
XX comprising a nucleic acid (a) encoding a PRO polypeptide, or its
XX extracellular domain (with or without its associated signal peptide),
XX which comprises any of the 275 120-850 residue amino acid sequences,
XX given in the specification; (b) comprising any of the 275 300-3500
XX nucleotide sequences, given in the specification; or (c) comprising the
XX full-length coding sequence of the nucleotide sequences given in the
XX specification, or of the DNA deposited under any of the American Type
XX Culture Collection (ATCC) Accession Numbers listed in the specification.
XX Also included are a vector comprising the novel nucleic acid, a host cell

PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US043956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001MO-US006560.
PR 01-MAR-2001; 2001US-00802706.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00860228.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001MO-US017800.
PR 14-JUN-2001; 2001US-00874503.
PR 19-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001MO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001MO-US020116.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

XX (GETH) GENENTECH INC.

XX Baker KP, Betesini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen MB, Goddard A, Godowski PJ, Gutney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
XX

DR MPI; 2003-331925/31.

P-PSDB; ABU66938.

XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
XX cancer.

XX Claim 2; Fig 185; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
CC extracellular domains and mature sequences, methods of detecting PRO
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of monocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release or proteoglycans from
CC cartilage, proliferation of inner ear utricular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of

CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIa, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. The present sequence encodes a PRO protein
CC of the invention

XX Sequence 1162 BP; 342 A; 266 C; 276 G; 278 T; 0 U; 0 Other;

Query Match 72.1%; Score 261.6; DB 8; Length 1162;
Best Local Similarity 56.6%; Pred. No. 7.9e-62;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

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Db 821 TACAGTTGACCTCCAGGAATTAATCTCGTCAATATTAAGAGAGAGCTGAAGTTGCCAAT 880
QY 121 GTNGTNTTYYTCCNMGTGYTYTYTNGTNCARNGNTGYGNGNAAATGYGNTGYGN 180
Db 881 GTGGCTTCTTTCACAGTGTGCTCCTCGTGACGAGCGGTGAGGAATGTGGCTGTGA 940
QY 181 ACGNTNAAATYGGMGWSNTGYACNTGYAATWSNGNAAACNGTNAARAAATATCAVAB 240
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QY 241 GTNTYTCARTTYGACGNGCAATYATTAABMNGMNGMNGNAAACATGAGCANTN 300
Db 1001 GTATTACGTTTGAGCTGGCCACATCAAGAGAGGGGTAGACTTAAGACATGAGCTTGA 1060
QY 301 GTNGAYATHCARYTNGAYCAAYCAVABMNTGYATGYATHTGYWSNWSMNGCNCN 360
Db 1061 GTTGACATCCAGTTGGATGATCAACATGACGATGATGATCTGAGAGCTCAAGACCACT 1120
QY 361 MG 362
Db 1121 CG 1122

Search completed: November 15, 2004, 15:09:02
Job time : -609.407 secs

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Db	868	GTNGTNTTYYTC	CNMGNTGYTNTYNTG	NCAMGNTGYG	GNCGNAAYTG	GGNTGYGN 927
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Db	988	GTNTYNTCAATTYGAAC	CNCGNCAIYATHAARMG	NGMGNGMGCNAABA	CNAATGCGNTYN	104
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RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	GI:29697257	DNA	linear	PAT 10-APR-2003
AR267254	AR267254	Sequence 6 from patent US 6495668.	AR267254	AR267254.1	GI:29697257			

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REFERENCE 1 (bases 1 to 1110)
AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
TITLE Growth factor homolog ZVEGF4
JOURNAL Patent: US 6495668-A 6 17-DEC-2002;
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Matches 362;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Dz

748 WSWTAYCAYGAYVGNAAARWSNAAARGTGNGAYTTNGAIVMGNVTNAAYGAYGCNAAARMGN 807

Dy 61 TAYWSNNGYACNCNMGNAAATYAYWSNGTNAAYATHMGARGARYTNARRYTNGCNAA 120
|||
Dd 808 TAYWSNTGYACNCNMGNAAATYAYWSNGTNAAYATHMGARGARYTNARRYTNGCNAA 867

121 GINGINITYTYTCMNGTGYNTYNGNCACBNGTGGGNGNAATYGGNTGYGN 180
 868 GINGINITYTYTCMNGTGYNTYNGNCACBNGTGGGNGNAATYGGNTGYGN 927

161 A A G N G I N A H I L G G M G M S N T G I A C N T G T A A Y M S N G G N A R A C N G T N A A A A R T A Y C A Y G A R 240
 928 A C N G T N A A Y T G G M G M S N T G T A C N T G T A A Y M S N G G N A R A C N G T N A A A R T A Y C A Y G A R 987

Db 988 GTNTTCARTTGGARCCGNCAYATTAARMGNGMNGMNCNMAPACNATGGCNYTN 1047

Db

1048 GTNGAYATHCARVTNGAYCAYGAGMGNTGYGAYTGATHTGYMSWMSNMGNCNCNCCN 1107

QY	361	MG	362
	1108	MG	1109
Db			

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	GI:11343347	1110 bp	DNA	linear	PAT 24-NOV-2000
AX0044492	AX0044492	Sequence 6 from Patent WO0066736.	AX0044492	AX0044492.1	GI:11343347				

ORGANISM
SOURCE
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1

AUTHORS Gilbertson, P.O. and Gilbertson, D.G.
TITLE Growth factor homolog vveg⁴
JOURNAL ZymoGenetics Inc (1994)
Patent: WO 0066736-A 6 09-NOV-2000;

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      location/Qualifiers
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/db_xref="taxon:32630"
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ORIGIN

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Query Match	72.1%	Score 261.6	DB 6	Length 1110
Best Local Similarity	100.0%	Pred. No. 4.3e-58		
Matches 362; Conservative	0	Mismatches	0	Indels 0
		Gaps	0	

Qy 1 MSNTATTCAGAYMGNRAARMSNAAGTNGAYTTNGAYMGNTTMAAYGAYGAYGCNAAPMGN 60
748 MSNTATTCAGAYMGNRAARMSNAAGTNGAYTTNGAYMGNTTMAAYGAYGAYGCNAAPMGN 807

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61	TAYASNTGGAACNCNMGNAAAYTAYWSNSNGNAAAYATHMGNGRGRARYTNAARYTNGCNAAAY 120
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Ddb

868 GINGNTTYYTCMNGTGYNYNYNGTNCARMGNTGGANGNAAATGCGGTGGCN 927

QY

121 GINGNTTYYTCMNGMTGYNYNYNGTNCARMGNTGGANGNAAATGCGGTGGCN 180

928 ACNGTNAAYTGGNGWMSNTGYACNTGYAAYWSNGGNAPARACNGTNAAPARTIYCAAYGAR 987

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VERSION
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DATE

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 Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis

JOURNAL Patent: WO 0208284-A 313 31-JAN-2002;

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Aubin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

FEATURES

Source location/Qualifiers

1. 1162

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ORIGIN

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Best Local Similarity 56.6%; Pred. No. 4.3e-58;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGAYMGNAARNSNARGTNGAYTNGAYMGNTTMAAYGAYGACNAARMGN 60

DB 761 TCATACCATGACCGGAAGTCAAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGCGT 820

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QY 121 GTNGTNTTYYTTCNMGNTGYTNTYNTGTCNARMGNTGYGNGNAAYTGCGNTGYGN 180

DB 881 GTGGCTCTCTTCCACGTTGCTCTCTCGTGACGCGCTGTGAGAGAAATGTGGCTGTGA 940

QY 181 ACGNTAAVTGGMGWSNTGYACNTGYAAVWSNGNNAARACNGTNAARATAYCAVGAR 240

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QY 241 GTNTYTCARTTYGARCNGNCAVATTHAARMGNMGNGMNGCNAAACATGCGNTYN 300

DB 1001 GTATTACAGTTTGAGCTCGGCACATCAAGAGAGGGGTAGAGCTTAAGACATGCTCTTA 1060

QY 301 GTNGAYATHCARYTNGAYCAVAYGARMGNTGYATGYATHTGYWSMWSMNGCNCCN 360

DB 1061 GTTGACATCCAGTTGATGATCAATGATGATGATGATGATGATGATGATGATGATGAT 1120

QY 361 MG 362

DB 1121 CG 1122

RESULT 5

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LOCUS Sequence 185 from Patent WO0140466.

AX464052

AX464052.1 GI:21899043

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis

JOURNAL Patent: WO 0208284-A 313 31-JAN-2002;

Genentech, Inc. (US)

FEATURES

Source location/Qualifiers

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ORIGIN

Query Match 72.1%; Score 261.6; DB 6; Length 1162;

Best Local Similarity 56.6%; Pred. No. 4.3e-58;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGAYMGNAARNSNARGTNGAYTNGAYMGNTTMAAYGAYGACNAARMGN 60

DB 761 TCATACCATGACCGGAAGTCAAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGCGT 820

QY 61 TAYNSNTGYACNCCMGNAAATYATWSNGTNAAYATMGNGARGARYTNAARYTNCNAY 120

DB 821 TACAGTTGACCTCCAGGAATTAATCTCGTCAATTAAGAGAAGAGCTGAAGTTGGCCAT 880

QY 121 GTNGTNTTYYTTCNMGNTGYTNTYNTGTCNARMGNTGYGNGNAAYTGCGNTGYGN 180

DB 881 GTGGCTCTCTTCCACGTTGCTCTCTCGTGACGCGCTGTGAGAGAAATGTGGCTGTGA 940

QY 181 ACGNTAAVTGGMGWSNTGYACNTGYAAVWSNGNNAARACNGTNAARATAYCAVGAR 240

DB 941 ACTGCAACTGAGAGTCTCGTCATGATGACGAGAAACCGTAAAGATATCATGAG 1000

QY 241 GTNTYTCARTTYGARCNGNCAVATTHAARMGNMGNGMNGCNAAACATGCGNTYN 300

DB 1001 GTATTACAGTTTGAGCTCGGCACATCAAGAGAGGGGTAGAGCTTAAGACATGCTCTTA 1060

QY 301 GTNGAYATHCARYTNGAYCAVAYGARMGNTGYATGYATHTGYWSMWSMNGCNCCN 360

DB 1061 GTTGACATCCAGTTGATGATCAATGATGATGATGATGATGATGATGATGATGATGAT 1120

QY 361 MG 362

DB 1121 CG 1122

RESULT 6

AX491206 1162 bp DNA linear PAT 16-AUG-2002

LOCUS Sequence 313 from Patent WO0200690.

AX491206

AX491206.1 GI:22323940

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis

JOURNAL Patent: WO 0200690-A 313 03-JAN-2002;

Genentech, Inc. (US)

FEATURES

Source location/Qualifiers

1. 1162

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 72.1%; Score 261.6; DB 6; Length 1162;

Best Local Similarity 56.6%; Pred. No. 4.3e-58;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGAYMGNAARNSNARGTNGAYTNGAYMGNTTMAAYGAYGACNAARMGN 60

Genentech Inc. (US)

location/Qualifiers

1. 1162

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 72.1%; Score 261.6; DB 6; Length 1162;

Best Local Similarity 56.6%; Pred. No. 4.3e-58;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGAYMGNAARNSNARGTNGAYTNGAYMGNTTMAAYGAYGACNAARMGN 60

DB 761 TCATACCATGACCGGAAGTCAAAAGTTGACCTGATGAGCTCAATGATGATGCCAAGCGT 820

QY 61 TAYNSNTGYACNCCMGNAAATYATWSNGTNAAYATMGNGARGARYTNAARYTNCNAY 120

DB 821 TACAGTTGACCTCCAGGAATTAATCTCGTCAATTAAGAGAAGAGCTGAAGTTGGCCAT 880

QY 121 GTNGTNTTYYTTCNMGNTGYTNTYNTGTCNARMGNTGYGNGNAAYTGCGNTGYGN 180

DB 881 GTGGCTCTCTTCCACGTTGCTCTCTCGTGACGCGCTGTGAGAGAAATGTGGCTGTGA 940

QY 181 ACGNTAAVTGGMGWSNTGYACNTGYAAVWSNGNNAARACNGTNAARATAYCAVGAR 240

DB 941 ACTGCAACTGAGAGTCTCGTCATGATGACGAGAAACCGTAAAGATATCATGAG 1000

QY 241 GTNTYTCARTTYGARCNGNCAVATTHAARMGNMGNGMNGCNAAACATGCGNTYN 300

DB 1001 GTATTACAGTTTGAGCTCGGCACATCAAGAGAGGGGTAGAGCTTAAGACATGCTCTTA 1060

QY 301 GTNGAYATHCARYTNGAYCAVAYGARMGNTGYATGYATHTGYWSMWSMNGCNCCN 360

DB 1061 GTTGACATCCAGTTGATGATCAATGATGATGATGATGATGATGATGATGATGATGAT 1120

QY 361 MG 362

DB 1121 CG 1122

RESULT 6

AX491206 1162 bp DNA linear PAT 16-AUG-2002

LOCUS Sequence 313 from Patent WO0200690.

AX491206

AX491206.1 GI:22323940

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis

JOURNAL Patent: WO 0200690-A 313 03-JAN-2002;

Genentech, Inc. (US)

FEATURES

Source location/Qualifiers

1. 1162

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 72.1%; Score 261.6; DB 6; Length 1162;

Best Local Similarity 56.6%; Pred. No. 4.3e-58;

Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 WSNATYCAVGAYMGNAARNSNARGTNGAYTNGAYMGNTTMAAYGAYGACNAARMGN 60

Db 761 TCATACATGACCGGAGAGTCAAAAGTGAAGTACGCTGATGAGCTCATGATGATGCTCAAGCCT 820
Qy 61 TATWSTNGYACNCCNMGNAAATYATWSTNGTAAATYTHMGNGARGARYTNAARYTNGCNAAY 120
Db 821 TACAGTTGACACTCCCGAGAAATTAATCGGTCAATATTAAGAAAGAGCTGAAGTTGGCCAAAT 880
Qy 121 GTNGTNTTYYTCNNMGNTGYTNTYNTGNCARMGNTGYGNGNGNAAYTGYGNTGYGNG 180
Db 881 GTGGTCTCTTTCACAGCTTCCCTGCTGCTGACGCTGAGAGGAAATGTGGCTGTGGA 940
Qy 181 ACGTNAATYTGNGMNSNTGYACNTGYAAVWSNGNAAACNGTNAARATYACAYGAR 240
Db 941 ACTGTCAACTGAGAGCTGCTGACATGCAATTCAGGAAAAACGTGAAAAAGTATCATGAG 1000
Qy 241 GTNTTCARTTYGACNCGNCAATYTHAARMGNGMNGNGCNAARACNAATGCGCTYTN 300
Db 1001 GTATTCAGATTGAGCTGCGCACATCAAGAGAGGGGTAGAGCTTAAGACCAATGGCTCTTA 1060
Qy 301 GTNGAYATHCARYTNGAYCAYCAYGARMGNTGYATGYATHTGYWSNMSNMNGCNCN 360
Db 1061 GTTGACATCCAGTTGATGATCAACATGAACATGCGATTGATCTGCAAGCTCAAGACCACT 1120
Qy 361 MG 362
Db 1121 CG 1122

RESULT 7
AY359116 1162 bp mRNA linear PRI 03-OCT-2003
DEFINITION Homo sapiens clone DNA94854 SCDGF-B (UNQ1899) mRNA, complete cds.
ACCESSION AY359116 GI:37183348
VERSION FLI CDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Gilmaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Kilmowski,D., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vandlen,R., Matanabe,C., Wieland,D., Woode,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1162)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
source
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA94854"
1..1162
/locus_tag="UNQ1899"
32..1126
/locus_tag="UNQ1899"
/note="PRO4345"
/codon_start=1
/product="SCDGF-B"
/protein_id="AAQ89474.1"

Query Match 72.1%; Score 261.6; DB 9; Length 1162;
Best Local Similarity 56.6%; Pred. No. 4.3e-58;
Matches 205; Conservative 91; Mismatches 60; Indels 0; Gaps 0;
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CRDPEVEDISETSTIRGRGCHREKVPRIKRTQIKITFSDDYFAKPEFKLY
YSLIEDPQPAASSTWSTSSISGVSYSPSYVDLTLADLADLKIAEFVDELL
KTFNPESVDELENNYLDTPRYRARSYHDKSKVDLRLDNDARVSCIPRANSVNR
ELKLANVFEPRCLIVORCGNGCCTVWRSCTCNSGATVKKYHEVLQFEPGHIR
RGRAKTALVDIQLDHERCDICSSRPSP"

Db 1 WSTNAYCAYGAYWMAARMAARGTGAYTNGAYVNGYNTNAAYGAYGAYNAARMG 60
Qy 761 TCATACATGACCGGAGAGTCAAAAGTGAAGTACGCTGATGAGCTCATGATGCTCAAGCCT 820
Db 61 TATWSTNGYACNCCNMGNAAATYATWSTNGTAAATYTHMGNGARGARYTNAARYTNGCNAAY 120
Qy 821 TACAGTTGACACTCCCGAGAAATTAATCGGTCAATATTAAGAAAGAGCTGAAGTTGGCCAAAT 880
Db 881 GTGGTCTCTTTCACAGCTTCCCTGCTGCTGACGCTGAGAGGAAATGTGGCTGTGGA 940
Qy 121 GTNGTNTTYYTCNNMGNTGYTNTYNTGNCARMGNTGYGNGNGNAAYTGYGNTGYGNG 180
Db 881 GTGGTCTCTTTCACAGCTTCCCTGCTGCTGACGCTGAGAGGAAATGTGGCTGTGGA 940
Qy 181 ACGTNAATYTGNGMNSNTGYACNTGYAAVWSNGNAAACNGTNAARATYACAYGAR 240
Db 941 ACTGTCAACTGAGAGCTGCTGACATGCAATTCAGGAAAAACGTGAAAAAGTATCATGAG 1000
Qy 241 GTNTTCARTTYGACNCGNCAATYTHAARMGNGMNGNGCNAARACNAATGCGCTYTN 300
Db 1001 GTATTCAGATTGAGCTGCGCACATCAAGAGAGGGGTAGAGCTTAAGACCAATGGCTCTTA 1060
Qy 301 GTNGAYATHCARYTNGAYCAYCAYGARMGNTGYATGYATHTGYWSNMSNMNGCNCN 360
Db 1061 GTTGACATCCAGTTGATGATCAACATGAACATGCGATTGATCTGCAAGCTCAAGACCACT 1120
Qy 361 MG 362
Db 1121 CG 1122

RESULT 8
AB033832 1428 bp mRNA linear PRI 10-FEB-2001
DEFINITION Homo sapiens hSCDGF-B mRNA for spinal cord-derived growth factor-B, complete cds.
ACCESSION AB033832
VERSION AB033832.1 GI:11602807
KEYWORDS spinal cord-derived growth factor-B; SCDGF-B.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hamada,T., Ui-Tel,K., Imaki,J. and Miyata,Y.
TITLE Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/EDGF-C/falotin
JOURNAL Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
PUBMED 11162582
REFERENCE 2 (bases 1 to 1428)
AUTHORS Hamada,T., Ui-Tel,K. and Miyata,Y.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology, 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5614-1684)
FEATURES
source
1..1428
/organism="Homo sapiens"
/mol_type="mRNA"

Oy		121	GTGCTTTTTCCTCCMGGTGGTATTTTGTCAGCAGTGGTGGAGAAATTGGCTGTGGA	180
Dd		693	GTTGGCTTCTTTTCCACCGTTGGCTCTCTGGTGCAGGCGTGTGAGAAATTGGCTGTGGA	752
Oy		181	ACNGTNAAYTGGMGMSNTGYACTGTGAAYWSNCGNNAAPACNGTNNABARTVCAVGAR	240
Dd		753	ACTGTCAACTGGAGAGTCTCTGCACATGTCCAATTTCAGGAAAACCGTGA AAAAAGTATCATGAG	812
Oy		241	GTNTTNCARTTYGARCCNGGNCAYATTAAMGMNGMNGMNCNAPACNATGGCNVTN	300
Dd		813	GTATTACAGTTTGAGCTGGGCCACATCAAGAAGAGGGGTAGAGCTTAAGACCATGGCTCTA	872
Oy		301	GTNGAVATHCARYTNGAYCAVCAYGARMENTGYCAATGYATHTGYSNMNMGNCCNCGN	360
Dd		873	GTTCGACATCCAGTTGATGCATCACATGAACGATGTGATATCTGCAGCTCAAGACCACCT	932
Oy		361	MG 362	
Dd		933	CG 934	
RESULT 11				
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LOCUS	AX704463			
DEFINITION	Sequence 3 from Patent WO02059618.			
ACCESSION	AX704463			
VERSION	AK704463.1	GI:29538586		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	Shinkler, R.A., Iichenstein, H., Herrmann, J.T., Bollog, F.T.,			
JOURNAL	Minkoff, S., Jeffers, M., Andrews, D. and Latochelle, W.			
FEATURES	Growth factor polypeptides and nucleic acids encoding same			
source	Patent: WO 02059618-A 3 01-AUG-2002; Curagen Corporation (US) Location/Qualifiers 1..1587 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"			
ORIGIN				
Query Match	72.1%; Score 261.6; DB 6; Length 1587;			
Best Local Similarity	56.6%; Pred. No. 4.6e-58;			
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;				
Oy		1	MSNTAYCAVGYVMGMAARMASNAARGTNGAYTTTNGATNGNYTNAAVYGVYGCNAAARMGN	60
Dd		573	TCATRCACATGACCGGAGAGTCAAAGGTGACCTGGATAGGCTCAATGATGATGCCAACGCT	632
Oy		61	TAYSNTGYACNCCMMGNAAYTAAWSNTGNAAYATHHGNGARGARYTNARVYMCNAAAY	120
Dd		633	TACAGTGCATCCCAAGAAATTACTCGGTCAATTAAGAGAAGAGCTGAAGTTGGCCAAAT	692
Oy		121	GTGCTTTTTCCTCCMGGTGGTATTTTGTCAGCAGTGGTGGAGAAATTGGCTGTGGA	180
Dd		693	GTTGGCTTCTTTTCCACCGTTGGCTCTCTGGTGCAGGCGTGTGAGAAATTGGCTGTGGA	752
Oy		181	ACNGTNAAYTGGMGMSNTGYACTGTGAAYWSNCGNNAAPACNGTNNABARTVCAVGAR	240
Dd		753	ACTGTCAACTGGAGAGTCTCTGCACATGTCCAATTTCAGGAAAACCGTGA AAAAAGTATCATGAG	812
Oy		241	GTNTTNCARTTYGARCCNGGNCAYATTAAMGMNGMNGMNCNAPACNATGGCNVTN	300
Dd		813	GTATTACAGTTTGAGCTGGGCCACATCAAGAAGAGGGGTAGAGCTTAAGACCATGGCTCTA	872
Oy		301	GTNGAVATHCARYTNGAYCAVCAYGARMENTGYCAATGYATHTGYSNMNMGNCCNCGN	360
Dd		873	GTTCGACATCCAGTTGATGCATCACATGAACGATGTGATATCTGCAGCTCAAGACCACCT	932
Oy		361	MG 362	
Dd		933	CG 934	

QY	361 MG 362	
Db	933 CG 934	
RESULT 12		
LOCUS	AX164744	1828 bp
DEFINITION	Sequence 1 from Patent WO0125437.	DNA
ACCESSION	AX164744	linear
VERSION	AX164744.1	PAT 22-JUN-2001
KEYWORDS	GI:14545598	
SOURCE		
ORGANISM	Homo sapiens (human)	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	Shmkeles R.A., Lichenstein H., Herrmann J.L., Boldog, F.L., Minskoff, S. and Jeffers, M.	
JOURNAL	Growth factor polypeptides and nucleic acids encoding same	
FEATURES	Patent: WO 0125437-A 1 12-Apr-2001; Curagen Corporation (US)	
source	Location/Qualifiers	
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Query Match	72.1%; Score 261.6; DB 6; Length 1828;	
Best Local Similarity	56.6%; Pred. No. 4,7e-58;	
Matches	205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;	
QY	1	WSNTRACAYGAMNNAARMSNAARGTNGAYTTNGAYMGNTNAAAYGAYGCNAARMGN 60
Db	929	TCATACATACATACCGGAAGTCMAAAGTGAAGCTGATAGGCTCAATGATGCAAGCGT 988
QY	61	TAYVSNITGYACNCCNMGNAAYTAYVMSNGTAAAYATMGNGARGARTNARATYNGCNAY 120
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Db	1049	GTGGTCTCTCTTCCAGGTGGCCCTCCGCGGACGCGCTGTGGAGAAATTGTGGCTGTGA 1108
QY	181	ACNGTNAAYTGYGWMNSNTGYACNTGYTAYVMSNGGAAACNGTNAARATRYCAYGR 240
Db	1109	ACTGTCAACGTGAGGCTCTGCAATGCAATTCAGGAGAAACCGTGAAGATATCATGAG 1168
QY	241	GTNTNCAITTYGARCCTGCAATTAARMGNGMNGMNGCNAARACNATGCGNTYT 300
Db	1169	GTATTCAGTTTGAAGCTGCGCACATCAAGAGAGAGGGTGAAGCTTAAGCCATGCTCTA 1228
QY	301	GTNGATATCATATNGAYCAYCAYGABMGNTGYATGATTTGYWSMNSMNGNCNCN 360
Db	1229	GTTCACATCCAGTTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1288
QY	361	MG 362
Db	1289	CG 1290
RESULT 13		
LOCUS	AX664403	1828 bp
DEFINITION	Sequence 3 from Patent WO02058716.	DNA
ACCESSION	AX664403	linear
VERSION	AX664403.1	PAT 24-MAR-2003
KEYWORDS	GI:29169373	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 Jeffers, M., Shinkets, R.A., Prayaga, S., Boldog, F.L., Yang, M.,
Burgess, C.E., Fernandez, E.R., Rietman, B., Shinkets, J.B.,
Laroche, W.J., and Lichenstein, H.S.
TITLE Treatment of inflammatory bowel disease using growth factors
JOURNAL Patent: WO 02058716-A 3 01-AUG-2002;
Curagen Corporation (US)
FEATURES location/Qualifiers
SOURCE 1. 1828
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 72.1%; Score 261.6; DB 6; Length 1828;
Best Local Similarity 56.6%; Pred. No. 4.7e-58;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 MSNTAYCAYGAYMGNAARMSNARGTNGAYTNGAYMNTNAYGAYGAYGNAARMGN 60
DB TCATACCATGACCGGAGATCAAAAGTTGACCTGATGAGCTCATGATGATGCCAAGCT 988
QY 61 TAYMNTGAYACNCCNMGNAAATYAYMNTNAYATMNGARGARYTNAARYTNGCNAAY 120
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QY 181 ACNGTNAAYTGMGMWNTGYACNTGYAYMNSNGNABACNGTNAARATATAYCAYGAR 240
DB ACTGCAACCTGAGAGCTGCTGCAATGCAATTCAGGAAACCGTGAAAGATCATGAG 1168
QY 241 GTNTNCAATTYGARGCCNGNCAATYATHAARMNGMNGMNGNCAACATGACNTYN 300
DB GTATTACAGTTTGAGCTCGGCAATCAAGAGAGGGGTAGAGCTAAGACATGGCTCTA 1228
QY 301 GTNGAYATHCARYTNGAYCAYCAYGARMNTGYATGYATHTGYMNSMNGNCNCCN 360
DB GTTGACATCCAGTTGATGATCACCATGAAAGATGATGTATCTGCACTCAAGACCACT 1288
QY 361 MG 362
DB 1289 CG 1290

RESULT 14
LOCUS AX704461 1828 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 1 from Patent WO02059618.
ACCESSION AX704461
VERSION AX704461.1 GI:29538585
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Shinkets, R.A., Lichenstein, H., Herrmann, J.L., Boldog, F.L.,
Mitschke, S., Jeffers, M., Andrews, D. and Laroche, W.
TITLE Growth factor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 02059618-A 1 01-AUG-2002;
Curagen Corporation (US)
FEATURES location/Qualifiers
SOURCE 1. 1828
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN
Query Match 72.1%; Score 261.6; DB 6; Length 1828;

Best Local Similarity 56.6%; Pred. No. 4.7e-58;
Matches 205; Conservative 97; Mismatches 60; Indels 0; Gaps 0;

QY 1 MSNTAYCAYGAYMGNAARMSNARGTNGAYTNGAYMNTNAYGAYGAYGNAARMGN 60
DB TCATACCATGACCGGAGATCAAAAGTTGACCTGATGAGCTCATGATGATGCCAAGCT 988
QY 61 TAYMNTGAYACNCCNMGNAAATYAYMNTNAYATMNGARGARYTNAARYTNGCNAAY 120
DB TACAGTTGACCTCCAGAGATTACTCGGTCAATATPAAGAAGAGCTGAAGTGGCCAT 1048
QY 121 GTNGTNTTYYTTCNMGNNTGYTNTNGTNCARMNTGYGNGNAAATGYGNTGYGN 180
DB GTGGCTCTTCTTCCACGTGCTCCTCGTGCAGCGCTGGAAGAAATGTGCTGTGGA 1108
QY 181 ACNGTNAAYTGMGMWNTGYACNTGYAYMNSNGNABACNGTNAARATATAYCAYGAR 240
DB ACTGCAACCTGAGAGCTGCTGCAATGCAATTCAGGAAACCGTGAAAGATCATGAG 1168
QY 241 GTNTNCAATTYGARGCCNGNCAATYATHAARMNGMNGMNGNCAACATGACNTYN 300
DB GTATTACAGTTTGAGCTCGGCAATCAAGAGAGGGGTAGAGCTAAGACATGGCTCTA 1228
QY 301 GTNGAYATHCARYTNGAYCAYCAYGARMNTGYATGYATHTGYMNSMNGNCNCCN 360
DB GTTGACATCCAGTTGATGATCACCATGAAAGATGATGTATCTGCACTCAAGACCACT 1288
QY 361 MG 362
DB 1289 CG 1290

RESULT 15
LOCUS AF335584 1828 bp mRNA linear PRI 24-APR-2001
DEFINITION Homo sapiens platelet-derived growth factor D mRNA, complete cds.
ACCESSION AF335584
VERSION AF335584.1 GI:13774335
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Laroche, W.J., Jeffers, M., McDonald, W.F., Chilikku, R.A.,
Giese, N.A., Lokker, N.A., Sullivan, C., Boldog, F.L., Yang, M.,
Vernet, C., Burgess, C.E., Fernandez, E., Deegler, L.L., Rietman, B.,
Shinkets, J., Shinkets, R.A., Rotberg, J.M., and Lichenstein, H.S.
TITLE PDGF-D, a new protease-activated growth factor
JOURNAL Nat. Cell Biol. 3 (5), 517-521 (2001)
MEDLINE 21231380
PUBMED 1131882
REFERENCE 2 (bases 1 to 1828)
Laroche, W.J., Jeffers, M., Yang, M., Vernet, C., Burgess, C.E.,
Fernandez, E., Shinkets, R.A. and Lichenstein, H.S.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Development, Curagen Corporation, 322 East
Main Street, Branford, CT 06405, USA
FEATURES location/Qualifiers
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/mol_type="mRNA"
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/chromosome="11"
/map="11q22.3"
/map="11q22.3"
/map="11q22.3"
/note="PDGF D"
/codon_start=1
/product="platelet-derived growth factor D"
/protein_id="AAK5840.1"
/db_xref="GI:13774335"
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 13:29:00 ; Search time 230.58 Seconds
(without alignments)
154.394 Million cell updates/sec

Title: US-09-876-813-2

Perfect score: 1994
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1988	99.7	370	2	JC7591
2	1775	89.0	370	2	JC7592
3	1737	87.1	370	2	JC7998
4	193	9.7	823	1	AS6788
5	189.5	9.5	707	2	JC2218
6	187.5	9.4	730	1	BMAU1
7	187.5	9.4	986	1	B58788
8	187.5	9.4	991	2	I49540
9	184.5	9.3	3623	2	T09456
10	176	8.8	927	1	JC0948
11	174.5	8.8	1057	1	A39288
12	173	8.7	3623	2	T08618
13	161	8.1	579	2	JC7629
14	156.5	7.8	1524	2	T30337
15	153	7.7	1464	2	S58984
16	149	7.5	1070	2	T31069
17	148	7.4	686	1	A59271
18	144	7.2	2403	2	A59386
19	143	7.2	699	1	I54763
20	141.5	7.1	767	2	T30018
21	138.5	6.9	1004	2	T30338
22	137.5	6.9	3871	2	T22812
23	137	6.9	276	2	A47290
24	136.5	6.8	449	2	A55362
25	136.5	6.8	597	2	S71352
26	134	6.7	705	1	JCHURB
27	130.5	6.5	402	2	JH0403
28	129	6.5	277	2	A41735
29	125.5	6.3	533	2	JC7985

30	123.5	6.2	275	2	JC6506	tumor necrosis fac
31	122.5	6.1	1290	2	A57190	ebnerin precursor
32	122	6.1	321	2	T33161	hypothetical prote
33	121	6.1	419	2	S69287	vascular endotheli
34	120.5	6.0	333	2	T21595	hypothetical prote
35	120	6.0	695	1	S05008	complement subcomp
36	118.5	5.9	1034	1	A53663	enteropeptidase (E
37	116.5	5.8	688	1	CIHUS	complement subcomp
38	116.5	5.8	1594	2	T30549	hensin - rabbit
39	114.5	5.7	1019	1	A56318	enteropeptidase (E
40	114.5	5.7	1035	1	A43090	enteropeptidase (E
41	113	5.7	504	2	S56745	mucin (clone pgm31
42	113	5.7	694	2	JC6554	complement subcomp
43	112	5.6	555	2	T21028	hypothetical prote
44	112	5.6	2083	2	T42721	CRP-ductin-alpha p
45	112	5.6	2197	2	B71600	variant-specific B

ALIGNMENTS

RESULT 1

JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7591
R:Hamada, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/
A:Reference number: JC7591, PMID:21092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-references: UNIPROT:Q9BWM5; UNIPROT:Q9GZP0; DDBJ:AB033832
C:Geneids:
A:Gene: scdGF-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:152-170/Region: CUB domain #status predicted
F:1272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F:1294-308/Region: conserved motif #status predicted

Query March	99.7%;	Score 1988;	DB 2;	Length 370;
Best local similarity	99.7%;	Pred. No. 1.3e-142;		
Matches 369;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MHRILFYVTLICANFCSCRDTSATPOSASIKALNNMLRDESNNLTDLYRDETIQYKG	60	
DB	1	MHRILFYVTLICANFCSCRDTSATPOSASIKALNNMLRDESNNLTDLYRDETIQYKG	60	
QY	61	NGYQSPFPNSYPRNLLTWRLHSQENTRIQLVFNQFGLEBENDICRYDFVEVDIS	120	
DB	61	NGYQSPFPNSYPRNLLTWRLHSQENTRIQLVFNQFGLEBENDICRYDFVEVDIS	120	
QY	121	ETSTIRGRMGCHKEVPRISRTNOIKTFKSDYFAKGFYIYSLDEFPAPASE	180	
DB	121	ETSTIRGRMGCHKEVPRISRTNOIKTFKSDYFAKGFYIYSLDEFPAPASE	180	
QY	181	TNMSVTSISISGVNSPSVTDPTLIADLDKTAEPDVEDLKYFNPESQWDLNNY	240	
DB	181	TNMSVTSISISGVNSPSVTDPTLIADLDKTAEPDVEDLKYFNPESQWDLNNY	240	
QY	241	LDTPRYGRSYHDKSKYVDLRLNDADKRYSCTPRNTSVNIREBKLANVFFPRCLIVQ	300	
DB	241	LDTPRYGRSYHDKSKYVDLRLNDADKRYSCTPRNTSVNIREBKLANVFFPRCLIVQ	300	
QY	301	RCGNCGCGTNNRSCNCSKTYKKEVLOFEPGHIKRRGRATMALVDIQLDHHRC	360	
DB	301	RCGNCGCGTNNRSCNCSKTYKKEVLOFEPGHIKRRGRATMALVDIQLDHHRC	360	
QY	361	DCICSSRPPR 370		
DB	361	DCICSSRPPR 370		

Db 361 DCICSSRPPR 370

RESULT 2

spinal cord-derived growth factor-B precursor - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07592

R/Hameda, T.; Uti-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A/Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/
A/Reference number: J07591; MIM:21092670; PMID:11162582

A/Contents: Fetal brain
A/Accession: J07592
A/Molecule type: mRNA
A/Residues: 1-370 <HAM>

A/Cross-references: UNIPROT:Q9EBQ1; DDBJ:AB052170
C/Genetics:
A/Gene: scdGF-B
F/1-17/Domain: secretory signal sequence #status predicted <SIG>
F/18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F/52-170/Region: CUB domain #status predicted
F/272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow
F/294-308/Region: conserved motif #status predicted

Query Match 89.0%; Score 1775; DB 2; Length 370;
Best Local Similarity 86.8%; Pred. No. 1.6e-126;
Matches 321; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFCSCDTSATPOSASIKALRNANLRDESNHLDLYRDETIQYKG 60
Db 1 MRLIVSLICANFCSCYDTPATPOSASIKALRNANLRDESNHLDLYRDENIQYTG 60

QY 61 NGVQSPRPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEVIS 120
Db 61 TGHVQSPRPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEVIS 120

QY 121 EFTIIRGRGCHKEVPRIRKSRNQIKTFKSDDYFAKPGFKIYSLIEDFQPAASE 180
Db 121 EFTIIRGRGCHKEVPRIRKSRNQIKTFKSDDYFAKPGFKIYSLIEDFQPAASE 180

QY 121 EFTIIRGRGCHKEVPRIRKSRNQIKTFKSDDYFAKPGFKIYSLIEDFQPAASE 180
Db 121 EFTIIRGRGCHKEVPRIRKSRNQIKTFKSDDYFAKPGFKIYSLIEDFQPAASE 180

QY 181 TMVESVTSISGVSYNSPSVTDPTLLADALDKIAEFDTVEDLKYFNPSWQDLENNY 240
Db 181 TMVESVTSISGVSYNSPSVTDPTLLADALDKIAEFDTVEDLKYFNPSWQDLENNY 240

QY 241 LDTPRYGRSYHDKRSKVDLRINDAKRYSCTPRNYSVINREBELKLANVFFPRCLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRINDAKRYSCTPRNYSVINREBELKLANVFFPRCLVQ 300

QY 301 RCGNGCGGTVMNRSCCTNSGKTYKKEVLOFEPGHIRKRGAKTMALVDIQLDHERC 360
Db 301 RCGNGCGGTVMNRSCCTNSGKTYKKEVLOFEPGHIRKRGAKTMALVDIQLDHERC 360

QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 3
JC7998
platelet-derived growth factor-D - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C/Accession: J07998

R/Zhuo, Y.; Hovle, G.W.; Zhang, J.; Morris, G.; Laeky, J.A.
Biochem. Biophys. Res. Commun. 308, 126-132, 2003
A/Title: A novel murine PDGF-D splicing variant results in significant differences in p
A/Reference number: J07998; PMID:12890490
A/Accession: J07998

A/Molecule type: mRNA
A/Residues: 1-370 <ZHU>
C/Comment: This protein is a potent mesenchymal cell mitogen and chemottractant involve

C/Genetics:
A/Gene: pdGF-D
A/Introns: 42/2; 110/1; 170/2; 191/2; 258/2; 330/1; 334/2
C/Keywords: fibroblasts; PDGF-D

Query Match 87.1%; Score 1737; DB 2; Length 370;
Best Local Similarity 85.1%; Pred. No. 1.2e-123;
Matches 315; Conservative 25; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRLIFVYTLICANFCSCDTSATPOSASIKALRNANLRDESNHLDLYRDETIQYKG 60
Db 1 MRLIVSLICANFCSCYDTPATPOSASIKALRNANLRDESNHLDLYRDENIQYTG 60

QY 61 NGVQSPRPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEVIS 120
Db 61 TGHVQSPRPNSYPRNLLTWRLHSGENTRIQLVFNQGLEAENDICRYDVEVEVIS 120

QY 121 EFTIIRGRGCHKEVPRIRKSRNQIKTFKSDDYFAKPGFKIYSLIEDFQPAASE 180
Db 121 EFTIIRGRGCHKEVPRIRKSRNQIKTFKSDDYFAKPGFKIYSLIEDFQPAASE 180

QY 181 TMVESVTSISGVSYNSPSVTDPTLLADALDKIAEFDTVEDLKYFNPSWQDLENNY 240
Db 181 TMVESVTSISGVSYNSPSVTDPTLLADALDKIAEFDTVEDLKYFNPSWQDLENNY 240

QY 241 LDTPRYGRSYHDKRSKVDLRINDAKRYSCTPRNYSVINREBELKLANVFFPRCLVQ 300
Db 241 LDTPRYGRSYHDKRSKVDLRINDAKRYSCTPRNYSVINREBELKLANVFFPRCLVQ 300

QY 301 RCGNGCGGTVMNRSCCTNSGKTYKKEVLOFEPGHIRKRGAKTMALVDIQLDHERC 360
Db 301 RCGNGCGGTVMNRSCCTNSGKTYKKEVLOFEPGHIRKRGAKTMALVDIQLDHERC 360

QY 361 DCICSSRPPR 370
Db 361 DCICSSRPPR 370

RESULT 4
A58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N/Alternate names: bone morphogenic protein splice form BMP-1/His
C/Species: Homo sapiens (man)
C/Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
A/Accession: A37278; MIM:158788

R/Mozney, J.M.; Rosen, V.; Celeste, A.J.; Mieleck, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1998
A/Title: Novel regulators of bone formation: molecular clones and activities.
A/Reference number: A37278; MIM:89072730; PMID:3201241

A/Accession: A37278
A/Molecule type: mRNA
A/Residues: 1-702; EKRPAQPRGRHQKFRYQKRRTPQ <MOZ>
A/Cross-references: GB:M22488; NID:9179499; PID:AAA51633.1; PID:9179500

R/Takahara, K.; Lyons, G.B.; Greenpan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A/Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (tm1d) are encode
A/Reference number: A58788; MIM:95096114; PMID:7798260

A/Accession: A58788
A/Molecule type: mRNA
A/Residues: 703-823 <TRK>
A/Cross-references: GB:L35278; NID:9619423; PID:AAAC1703.1; PID:9619424

C/Genetics:
A/Gene: GDB:BMP-1
A/Cross-references: GDB:125203; OMIM:112264
A/Map position: 8p21-8p21

C/Function:
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
A/Supernatant: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; EC
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F/130-321/Domain: astacin homology <AST>
F/322-431/Domain: C1r/C1s repeat homology <C1R1>

Tue Nov 16 16:09:43 2004

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F/435-544/Domain: C1r/C1s repeat homology <C1R2>
F/551-587/Domain: EGF homology <EGF>
F/591-700/Domain: C1r/C1s repeat homology <C1R3>
F/738-752/Region: histidine-rich
F/911-142,333,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F/213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
F/214/Active site: Glu #status predicted
F/556/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match          9.7%; Score 193; DB 1; Length 823;
Best Local Similarity 28.7%; Pred. No. 1.5e-06;
Matches 71; Conservative 33; Mismatches 89; Indels 54; Gaps 11;

Qy 59 KGNVGVSPRPNSYPRLLLTWRLHSGENTRIQLVFPNQGLEAENDICRYDFVEVD 118
Db 597 KLNQSIISPGWPKFEPKNCIMQVLVAPTYRISLQFD--PFETEGNDVCKYDFVEVRS 653

Qy 119 ISETSTIRGWCCHKEVPPRIKSRITQIKITFKSDDYFVAKPGFKI-YYSILE----- 171
Db 654 GLTDSKLGKFCG-SERKEVITSGYNNMRVEFKSDN-TVSKKGKAFPSVLBAGDRH 711

Qy 172 -----DPPAASETNWEVSSTSGVSYNSPVTD---PTLIADLD 211
Db 712 SHLSGLIELLCPHALVDTPAPPSALHGDTHAHHTHTHCPIAQETCRGEPILGASRLS 771

Qy 212 KKIAEFDVEDLTKFPESQEDLENNYLD-TPYRGSRVHDKSKYDLRLINDADRY 270
Db 772 PQGEGHLLTA-----PQ-----EGSYLDFPDWTHRG---DPKPR---RRRKSILTF 810

Qy 271 SCTPRNY 277
Db 811 SLTPATF 817

RESULT 5
JC2218
N:Collagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C/Accession: JC2218
R/Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A>Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
A:Reference numbers: JC2218; MUID:94085787; PMID:8262384
A/Accession: JC2218
A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: UNIPROT:P98070; GB:L12249; NID:9406540; PIDD:AAA16313.1; PID:9406541
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; F
C/Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F/93-284/Domain: ascatin homology <AST>
F/285-397/Region: complement 1r/1s-like repeat
F/285-394/Domain: C1r/C1s repeat homology <C1R1>
F/398-510/Region: complement 1r/1s-like repeat
F/398-507/Domain: C1r/C1s repeat homology <C1R2>
F/514-550/Domain: EGF homology <EGF>
F/554-666/Region: complement 1r/1s-like repeat
F/554-663/Domain: C1r/C1s repeat homology <C1R3>
F/62,109,235,336/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/116,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F/177/Active site: Glu #status predicted
F/528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match          9.5%; Score 189.5; DB 2; Length 707;
Best Local Similarity 42.5%; Pred. No. 2.2e-06;
Matches 45; Conservative 18; Mismatches 38; Indels 5; Gaps 4;

Qy 59 KGNVGVSPRPNSYPRLLLTWRLHSGENTRIQLVFPNQGLEAENDICRYDFVEVD 118
Db 560 KLNQSIISPGWPKFEPKNCIMQVLVAPTYRISLQFD--PFETEGNDVCKYDFVEVRS 616

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Qy 119 ISETSTIRGWCCHKEVPPRIKSRITQIKITFKSDDYFVAKPGFK 164
Db 617 GLTDSKLGKFCG-SELPAVITSGYNNMRVEFKSDN-TVSKKGQ 660

RESULT 6
BMHUI
N:Collagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
A:Alternate names: bone morphogenic protein 1 (BMP1)
C:Species: Homo sapiens (man)
C>Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C/Accession: A37278; B58788
R/Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mitsuoka, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A>Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference numbers: A37278; MUID:89072730; PMID:3201241
A/Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-730 <MOZ>
A:Cross-references: GB:M22488; NID:g179499; PIDD:AAA51833.1; PID:g179500
C:Genetic: GDB:BMP1
A:Gene: GDB:BMP1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A>Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; E
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
F/1-32/Domain: signal sequence #status predicted <SIG>
F/23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F/130-331/Domain: ascatin homology <AST>
F/332-431/Domain: C1r/C1s repeat homology <C1R1>
F/435-544/Domain: C1r/C1s repeat homology <C1R2>
F/551-587/Domain: EGF homology <EGF>
F/551-587/Domain: C1r/C1s repeat homology <C1R3>
F/91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
F/213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F/214/Active site: Glu #status predicted
F/565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match          9.4%; Score 187.5; DB 1; Length 730;
Best Local Similarity 39.4%; Pred. No. 3.3e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

Qy 59 KGNVGVSPRPNSYPRLLLTWRLHSGENTRIQLVFPNQGLEAENDICRYDFVEVD 118
Db 597 KLNQSIISPGWPKFEPKNCIMQVLVAPTYRISLQFD--PFETEGNDVCKYDFVEVRS 653

Qy 119 ISETSTIRGWCCHKEVPPRIKSRITQIKITFKSDDYFVAKPGFKIY 167
Db 654 GLTDSKLGKFCG-SERKEVITSGYNNMRVEFKSDN-TVSKKGKAF 700

RESULT 7
B58788
N:Collagen C-endopeptidase (EC 3.4.24.19) precursor, collagen-like splice form - human
A:Alternate names: bone morphogenic protein 1, collagen-like splice form
C:Species: Homo sapiens (man)
C>Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
C/Accession: A37278; B58788
R/Mooney, J.M.; Rosen, V.; Celeste, A.J.; Mitsuoka, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A>Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference numbers: A37278; MUID:89072730; PMID:3201241
A/Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, 'EKPPALQPRGPHQIKERVQKRNTPQ' <MOZ>
A:Cross-references: UNIPROT:P1497; GB:M22488; NID:g179499; PIDD:AAA51833.1; PID:g179500
R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A>Title: Bone morphogenetic protein-1 and a mammalian collagen-like domain (mTld) are encoded

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A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: B58788
A:Molecule type: mRNA
A:Residues: 703-986 <TAK>
A:Cross-references: GB:IJ35279; NID:g619860; PIDN:AA41710.1; PID:g619861
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:I25203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A>Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type C.
C:Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; F.
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g.
F:1-22/Domain: signal sequence #status predicted <SIG>
F:130-986/Product: procollagen C-endopeptidase tollold-like splice form #status predicted
F:130-321/Domain: astacin homology <AST>
F:122-431/Domain: Clr/Cls repeat homology <CLR1>
F:435-544/Domain: Clr/Cls repeat homology <CLR2>
F:551-587/Domain: EGF homology <EG1>
F:591-700/Domain: Clr/Cls repeat homology <CLR3>
F:707-742/Domain: EGF homology <EG2>
F:747-856/Domain: Clr/Cls repeat homology <CLR4>
F:860-973/Domain: Clr/Cls repeat homology <CLR5>
F:1142,332,363,559/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:63-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-664/Binding site: zinc (His, His, Tyr) #status predicted
F:213,217,222,272/Binding site: zinc (His, His, Tyr) #status predicted
F:565,720/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted

Query Match 9.4%; Score 187.5; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 4.8e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

QY 59 KANGYVOSPRFPNSYPNNLLTWRLHSGENTRIQLVPDNGGLEAENDICRDPFEVED 118
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Dbp KLNGSITSPGMPKKEPPPKNCIQCWVAPEYRISLQFP--FFTEGNDVCXIDFVEVR 653
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 119 ISETSTIRGMCGHKVEYPPRIKSRTNOIKTFPSDDYFAKPGFKTY 167
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 654 GLTDASKLHGRCG-SSEKREVITSQYNMRVFEKSDN-TYSKKGFKAHF 700
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 8
149540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollold-like splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49540
R:Fukagawa, M.; Noboru, S.; Hognan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A>Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A:Reference number: I49540; MUID:94229342; PMID:8174772
A:Accession: I49540
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
C:Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C:Genetics:
A:Gene: Bmp-1
C:Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; E
C:Keywords: hydrolyase; metalloproteinase; zinc
F:135-326/Domain: astacin homology <AST>
F:556-592/Domain: EGF homology <EG1>
F:596-705/Domain: Clr/Cls repeat homology <CLR>
F:712-747/Domain: EGF homology <EG2>
F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F:219/Active site: Glu #status predicted

Query Match 9.4%; Score 187.5; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 4.9e-06;
Matches 43; Conservative 18; Mismatches 43; Indels 5; Gaps 3;

59 KANGYVOSPRFPNSYPNNLLTWRLHSGENTRIQLVPDNGGLEAENDICRDPFEVED 118

Db 602 KLNGSITSPMPKEXEPYNNKNCIMQLVAPTYGRISLQFD---FFLEGNDVCKYDPVEVRS 658

Qy 119 ISESTIIIRRMCGHKEVPRRIKSRNTQIKITFSDDYFAKPKFKIY 167

Db 659 GLTADSGLHGKFCG-SEKPEVITSQYNNMRVEFKSDN-TVSKKGFKAF 705

RESULT 9

T09456

Intrinsic factor-B12 receptor Cubilin precursor - human

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T09456

R/Kozuyaki, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N

Blood 91, 3593-3600, 1998

A/Title: The human intrinsic factor-Vitamin B12 receptor, cubilin: Molecular characterization.

A/Reference number: Z16677; MIMD:98241400; PMID:9572993

A/Accession: T09456

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-3623 <KOZ>

A/Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:G3929528; PIDD:AAC82612.1; PID:G33333

C/Genetics:

A/Map position: 10p12

C/Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology

C/Keywords: receptor; vitamin B12 uptake

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>

F/436-467/Domain: EGF homology <EGF>

Query Match 9.3%; Score 184.5; DB 2; Length 3623;

Best Local Similarity 24.3%; Pred. No. 4,4e-05;

Matches 85; Conservative 34; Mismatches 120; Indels 111; Gaps 17;

Qy 56 IGVKNGVQSDPRFNSPYRNLLTWRLHSEOENTRIQLVFNQFGEAENDICRYDFVE 115

Db 935 ILTESIGTIQSGHPRVYHGINCTWHILVQPHLHMFET-FHLEPHN--CTNDYLE 991

Qy 116 VEDI-SETSTITRGMCGHKEVPRRIKSRNTQIKITFKSDDYVANKPKFIY----- 167

Db 992 YVDITSETSL---GRYCG-KSIPPSLTSGNSIMLFFVTD- DLAVEGLFNYEAI SAT 1046

Qy 168 SLIEDFOPAAASET-----WESVTSSISGSVNSPSVTDPTLADALDKIAEF 217

Db 1047 ACLQYITDLDLGTFFPNPNPNPNNECI-----YRI-TVRGQLA----- 1087

Qy 218 DTVEDLKYFNESWQEDLENNYLDTPRYGRSY-----HDKR-- 255

Db 1088 -----VHFTFSLSEAIAGNYTDFLEIRDGYEKSLGIFGSLNPPTIISHSKLM 1140

Qy 286 SKVDLRINDAKRYSCTPRNYSVNIRELKLANVFFPRCLLVORCGNGCGGYNNRS 315

Db 1141 LKFKSDQI-DTRSGSAYWDGSGTG-----CGGN----- 1168

Qy 316 CTNSGKTVKKYHEVLQEPGHI-----KRGRAKTMALVDIQLDHNRC 360

Db 1169 LTTSGGTISPNYPMYPYHSSECYWMLKSHSASAELEFKDPHLEHHPNC 1218

RESULT 10

J00948

As antigen precursor - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C/Accession: J00948

R/Takagi, S.; Hizata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.

Neuron 7, 285-307, 1991

A/Title: The As antigen, a candidate for the neuronal recognition molecule, has homology

A/Reference number: J00466; MUID:91337458; PMID:1908252

A/Accession: J00466

A/Molecule type: mRNA

RESULT 11
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A39288
R/Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A/Title: The *Drosophila* dorsal-ventral patterning gene tolloid is related to human bone
A/Reference number: A39288; MUID:92034970; PMID:1840509
A/Accession: A39288
A/Stratus: preliminary
A/Molecule type: mRNA
A/Releides: 1-1057 <SHI>
A/Cross-references: UNIPROT:P25723; GB:M76976; NID:9157305; PID:AAA28491.1; PID:915730606
C/Genetics:
A/Gene: FlyBase:tlid
A/Cross-references: FlyBase:FBgn0003719
C/Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeats
C/Keywords: duplication; hydrolase; metalloproteinase; zinc
F/136-329/Domain: astacin homology <ASr>
F/352-464/Domain: C1r/C1s repeat homology <C1R1>
F/468-578/Domain: C1r/C1s repeat homology <C1R2>
F/585-620/Domain: EGF homology <EG1>
F/624-740/Domain: C1r/C1s repeat homology <C1R3>
F/747-782/Domain: EGF homology <EG2>
F/787-896/Domain: C1r/C1s repeat homology <C1R4>
F/920-1013/Domain: C1r/C1s repeat homology <C1R5>
E/221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
E/222/Active site: Glu #status predicted

Query Match 8.7%; Score 173; DB 2; Length 3623;
Best Local Similarity 26.4%; Pred. No. 0.00033;
Matches 62; Conservative 35; Mismatches 98; Indels 40; Gaps 10;

15 PCSCDTSATPPOSASIKALRNANLRDSEHNLVDLVRDE----TIQVKGNGVQSPRP 70
Db FCSNIPSPFTSVYNLLVYTPVKSSSMENNGFPAKSSDLCEGEVLTASTGIIESP 949
QY NSYPNNLLTWMLHSOENTRIOLVFNNOGLAEANDICRYDFEVEDISTETIIRGRW 130
Db NVPYPGVNMCTMVAVVQROGLIRLF--SSFLERHYN--CINDYIEITDTAAQTL--GRY 1004
QY CGHKEVPPRIKSRINOIKITPKSDDYFVAPKGFRIYSLLEDFOPAAAS----- 179
Db CG-KSIPSPSLTNSNSNIKLIFVSDS--ALAHGEFSINYEALD-----ASSVCLYDVTNMG 1057
QY 180 -----ETWESVTSISGSVSN-SPSTVTDPTLIDALDALKTAEPVTEV 222
Db 1058 MLSSPNNPNNYSSNNECIYRITVGLNQOIALHFTDFTL-EDYFGSQCVDFEIRD 1111

RESULT 12

T08618
intrinsic factor-B12 receptor CUBILIN precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R:Accession: T08618
R:Mostrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayser, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A:Reference number: Z16459; MUID:98148073; PMID:9478979
A:Accession: T08618
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-3623 <MOE>
A:Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:G3834379; PIDN:AAC71661.1; PID:G3
C:Genetics:
A:Gene: CUBILIN
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane;
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F:133-164/Domain: EGF homology <EGF1>
F:436-467/Domain: EGF homology <EGF>

Query Match 8.7%; Score 173; DB 2; Length 3623;
Best Local Similarity 26.4%; Pred. No. 0.00033;
Matches 62; Conservative 35; Mismatches 98; Indels 40; Gaps 10;

15 PCSCDTSATPPOSASIKALRNANLRDSEHNLVDLVRDE----TIQVKGNGVQSPRP 70
Db FCSNIPSPFTSVYNLLVYTPVKSSSMENNGFPAKSSDLCEGEVLTASTGIIESP 949
QY NSYPNNLLTWMLHSOENTRIOLVFNNOGLAEANDICRYDFEVEDISTETIIRGRW 130
Db NVPYPGVNMCTMVAVVQROGLIRLF--SSFLERHYN--CINDYIEITDTAAQTL--GRY 1004
QY CGHKEVPPRIKSRINOIKITPKSDDYFVAPKGFRIYSLLEDFOPAAAS----- 179
Db CG-KSIPSPSLTNSNSNIKLIFVSDS--ALAHGEFSINYEALD-----ASSVCLYDVTNMG 1057
QY 180 -----ETWESVTSISGSVSN-SPSTVTDPTLIDALDALKTAEPVTEV 222
Db 1058 MLSSPNNPNNYSSNNECIYRITVGLNQOIALHFTDFTL-EDYFGSQCVDFEIRD 1111

RESULT 13

membrane-type frizzled-related protein - human

C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JCT629
R:Kato, M.
Biochem. Biophys. Res. Commun. 282, 116-123, 2001
A:Title: Molecular cloning and characterization of MRP, a novel gene encoding a membran
A:Reference number: JCT629; MUID:21164708; PMID:11263980
A:Accession: JCT629
A:Molecule type: mRNA
A:Residues: 1-579 <RAT>
A:Cross-references: UNIPROT:Q9BY79; DDBJ:AB055505
C:Comment: This protein, which plays key roles in medulla oblongata as a regulator of th
ubulin domains.
C:Genetics:
A:Gene: mrip
A:Map position: 11q23
A:Keyword: transmembrane protein

Query Match 8.1%; Score 161; DB 2; Length 579;
Best Local Similarity 26.2%; Pred. No. 0.00024;
Matches 49; Conservative 29; Mismatches 63; Indels 46; Gaps 9;

QY 11 ICANFSCGDTATPQSASIKALRNANLRDESN-----HLDLYRDETITQYKG 60
DB 278 VCDGFANCAQGS-----DETNCSAKFGGCGNLTGL----- 308

QY 61 NGYVSPREPNSYPNNLLTWRLHSGENTRIQVFDNPGLEAENDICRYDFVEVEDIS 120
DB 309 QGTFSRPSYLTQYPHQLCTWHISVPAGHSIELQHN-FSLF-AQDECKPDYEVYETS 365

QY 121 EISTT-IRRMCGHKEVPPRIKSRINOIKITPKSDYVNAKPGFKIYSLLEDPO-PAAA 178
DB 366 SSGASFLGRFCG-AEPPHVLVSHHELAFLVRL-DHGISSGGSFATYLAFTNATENPCGP 423

QY 179 SETNWS 185
DB 424 SETLSCQA 430

RESULT 14
T30337
polyprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30337
R:Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from X
A:Reference number: Z20829
A:Accession: T30337
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1524 <YAN>
A:Cross-references: UNIPROT:Q91674; EMBL:U81290; NID:q2981640; PID:g2981641; PIDN:AA0247
C:Superfamily: tyrosin related polypeptide; trypsin homology

Query Match 7.8%; Score 156.5; DB 2; Length 1524;
Best Local Similarity 26.1%; Pred. No. 0.0019;
Matches 54; Conservative 36; Mismatches 72; Indels 45; Gaps 10;

QY 58 VKNGYVQSPRPSPNSYPNNLLTWRLHSGENTRIQVFDNPGLEAENDICRYDFVEVE 117
DB 435 LKKGMITSPNYPDPYRLKTCWIIIEPENNIVLKFED-FNVEYGHG--CIYDAVEYV 491

QY 118 DISETSTIIRMGCGHKEVPPRIKSRINOIKITPKSD---DYFAKPGFKI----- 165
DB 492 DGAEEKQLI-ARLCGY-TLPPISSPENTMIRKTIEMNSY----PGFKVKSFPVPEK 545

QY 166 YVSLLEPQPAASSETWESVTSISGVSYNSPVTDPTLIADALDKIAEFPTVEDLK 225
DB 546 QPSPVVDTP-TISMLPRAIALDVCGMAPWTPEKMLPRIVG-----E 588

QY 226 YFNESWQEDLENNYLTDPYRGRSYH 252

DB 569 EASPSWPMQVQIRFL-----RTFH 608

RESULT 15
S58984
development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S58984
R:Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
Genetics 141, 271-281, 1995
A:Title: The tolkin gene is a tollold/BMP-1 homologue that is essential for Drosophila de
A:Reference number: S58984; MUID:96042912; PMID:8536976
A:Accession: S58984
A:Molecule type: mRNA
A:Residues: 1-1464 <FIN>
A:Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:g1002985; PIDN:AA047015.1; PID:g100;
A>Note: the authors did not translate the codon for residue 722
C:Genetics:
A:Gene: tolkin
A:Cross-references: FlyBase:FBgn0004885
C:Keywords: hydrolase; metalloproteinase; zinc
F:529-722/Domain: ascacin homology <AST>
F:958-993/Domain: EGF homology <EGF>
F:118-1153/Domain: EGF homology <EGF1>
F:614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predicted
F:615/Active site: Glu #status predicted

Query Match 7.7%; Score 153; DB 2; Length 1464;
Best Local Similarity 24.8%; Pred. No. 0.0033;
Matches 57; Conservative 27; Mismatches 60; Indels 86; Gaps 9;

QY 5 IFYITLICAN-----FSCGRTSATPQSASIKALRNANLRDESNHLDLYRDETITQ 57
DB 1059 VTVYSKLGENTRLKRIGFCG---SSIPPTAT-----SESNALRLFEHSDKSIQ 1103

QY 58 VKG-----NGY----- 63

DB 1104 RSGFAVFPFDIDECVANNNGGCOHECRNTGTYICMCHNGYSMHENHNDCKECKEYETS 1163

QY 64 -----VQSPRPSPNSYPNNLLTWRLHSGENTRIQVFDNPGLEAENDICRYDFVEVED 118
DB 1164 APFGTIFSPNYPDPYRLKTCWIIIEPENNIVLKFED-FNVEYGHG--CIYDAVEYV 1220

QY 119 ISETSTIIRMGCGHKEVPPRIKSRINOIKITPKSDYVNAKPGFKIYSLLEDPO-PAAA 168
DB 1221 GSESSSVLGRFCGDK-IPFPISSSTSNOMYVWLKTDKN-KQKNGFTASHS 1268

Search completed: November 15, 2004, 13:58:15
Job time : 231.58 secs